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-LOOPGXI=0
-DATIZ=b116 -STRAT=1 -RND=-1 -MATRIX=b108um62 -TRANS=human40.cdi -LIGS=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -TRR_MN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMI=pct -NORM=ext -HEAPSIZE=500 -MINIENS=0 -MAXIENS=2000000000
-USER=US09444281 @CGN 1 1 3608 @runat 07052004 171138 2568 -NCPU=6 -ICPU=3
-NO MAAP -LIARGEQUERY -NEG SCORES=0 -WAIT -DSPBICCK=100 -LONGICG
-DBV TINEOUT=120 -WARN TIMBOUT=30 - TRREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                      May 11, 2004, 13:53:18; Search time 2407.08 Seconds (without alignments) 234.084 Million cell updates/sec
               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                      OM protein - nucleic search, using frame plus p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                           Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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1: 9b ba:*

2: 9b htg:*

4: 9b om:*

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9: 9b pat:*

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BD247529.1 GT:33057299
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8 SYNThetic construct
SYNThetic construct
A strificial sequences.
E I (bases I to 114)
Burian, J. and Bartfeld, D.
Method for effectively producing antibacterial cationic peptides in host cells.
E A sequence CONSTRUCT INC.
OST ARTIFICIAL SEQUENCE INC.
OST ARTIFICIAL SEQUENCE INC.
OST ARTIFICIAL SEQUENCE
EN UP 2002530114-A/23
ED 17-SEP-2002
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BD247529
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JAN BURIAN, DANIEL BARTFELD
CI2N15/09, C07K1/12, C07K1/18, C12N1/15, C12N1/19, C12N1/21, C12P21/
   C12N15/09, C07K1/12, C07K1/18, C12N1/15, C12N1/19, C12N1/21, C12P21/
                                                Кеу
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Synthesized oligonucleotide used as a template for PCR
Location/Qualifiers
                                            Synthesized oligonucleotide us as a template for PCR Location/Qualifiers
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                                                                                         organism='Artificial Sequence'.
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Conservative:
Mismatches:
Indels:
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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1. .108
/organism="synthetic construct"
/mol_type="qenomic DNA"
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BD247529
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                                                                  BD247517.1 GI:33057287
DP 2002530114-A/11.
Synthetic construct
Synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 114)
Burian, J. and Bartfeld, D.
Method for effectively producing antibacterial cationic peptides in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic construct
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 108)
Burlan,J. and Bartfeld,D.
Method for effectively producing antibacterial cationic peptides in
                                                                                                                                                                                                                                Artificial Sequence
JP 2002530114-A/11
JP 2002530114-A/11
19-NOV-1999 UP 2000584088
20-NOV-1999 US 60/109218
JAN BURIAN, DANIEL BARTEELD
C12N15/09,C07R1/12,C07R1/18,C12N1/15,C12N1/19,C12N1/21,C12P21/
               BD247517 17-JUL-2003
Method for effectively producing antibacterial cationic peptides in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BD247523 108 bp DNA linear PAT 17-JUL-2003 Method for effectively producing antibacterial cationic peptides in Host calls.
                                                                                                                                                                                                                                                                                                                                                                      Synthesized oligonucleotide used as a template for PCR FH Location/Qualifiers source 1. .114
                                                                                                                                                                                                                                                                                                                                                                                                              /organism='Artificial Sequence' Location/Qualifiers
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13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:

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                                                                                                                                                                                                      Patent: JP 2002530114-A 11 17-SEP-2002;
MICROLOGIX BIOTECH INC
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MICROLOGIX BIOTECH INC
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(C12P21/02,C12R1:19),C12N15/00
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JP 2002530114-A/17
17-SEP-2002
19-NVV-1999 JP 2000584088
20-NVV-1998 US 60/109218
JAN BURIAN, DANIEL BARTFELD
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JP 2002530114-A/17.
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Best Local Similarity:
Query Match:
DB:
                                         lost cells.
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BD247517
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Score:

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Key

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Bylina, B.J., Coleman, W.J. and Youvan, D.C.
High-throughput methods for generating and screening compounds that
affect cell viability
Patent: WO 24-JAN-2002;
Rairos Scientific, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT 13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
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                                          28-MAY-1998 JP 1999500514
28-MAY-1997 KR 1997/21312,09-APR-1998 KR 1998/13372 PI
CHANG KIM, JAE HYUN LEE, MIN HYUNG KANG, JEONG HYUN KIM, SEUNG
                                                                                                  HYDN SOO LEE
C12N15/62
Method for mass production of antimicrobial peptide FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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/organism='Indolicidin gene'
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Conservative:
Mismatches:
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Mismatches:
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Sequence 6 from Patent W00206517,
AX357080

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                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AAATGGCCGTGGTGGCCGTGGCGTCGT 39
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                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                      Location/Qualifiers
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JP 2002502246-A/15
22-JAN-2002
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artificial sequences.
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73.00
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Best Local Similarity: 1
Query Match:
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Best Local Similarity:
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VERSION
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AUTHORS
TITLE
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                                                                                                                                                                                                                          artificial sequences.

1 (bases 1 to 151)

Buriah, J. and Bartfeld, D.

Method! for effectively producing antibacterial cationic peptides in host cells

Patent: JP 2002530114-A 14 17-SEP-2002;

MICROLOGIX BIOTECH INC

OS Artificial Sequence

PP 17-SEP-2002

PP 17-SEP-2002
                                                                                                              BD247520 151 bp DNA linear PAT 17-JUL-2003 Method for effectively producing antibacterial cationic peptides in
                                                                                                                                                                                                                                                                                                                                                                    19-NOV-1999 JP 2000584088
20-NOV-1998 US 60/109218
JAN BURIAN, DANIEL BARTFELD
CIZNIS/09, COTKL/12, COTKL/18, CIZNI/15, CIZNI/19, CIZNI/21, CIZP21/
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Kim,S.C., Lee,J.H., Kang,M.H., Kim,J.H., Hong,S.S. and Lee,H.S.
Method for mass production of antimicrobial peptide
Patent: JP 2002502246-A 15 22-JAN-2002;
SANYANG GENEX CORP, KOREA ADVANCED INSTITUTE OF SCIENCE AND
TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                        (C12P21/02,C12R1:19),C12N15/00
Synthesized oligonucleotide used as a template for PCR
Location/Qualifiers
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                                                44 ATGATTCTGCGTTGGCCGTGGCCGTGGCGTCGCAAA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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Indels:
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    US-09-444-281-35 (1-13) x BD247529 (1-114)
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JP 2002502246-A/15.
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                                                                                                                                                                                                 synthetic construct
synthetic construct
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unidentified
unclassified
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ORGANISM
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TITLE
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BD128612
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RESULT 7
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KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS TITLE

source

JOURNAL

FEATURES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Del Sal,G., Storici,P., Schneider,C., Romeo,D. and Zanetti,M. orgNR cioning of the neutrophil bactericidal peptide indolicidin Biochem. Biophys. Res. Commun. 187 (1), 467-472 (1992) 92392368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Del Sal,G.
Del Sal,G.
Direct Submission
Submitted (20-ULL-1992) G. Del Sal, Univ. of Trieste, Dip. di
Blochimica, Biofisica e Chimica, delle Macromolecole, Via A.
Valerio, 38, 34127 Trieste, ITALY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X67340.1 G1:462
cathelicidin, CATHL4 gene, indolicidin antimicrobial peptide.
Bos taurus (cow)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13. .447

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/kuntion="indolicidin antimicrobial peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                            את 550 bp mRNA line
Bos taurus mRNA for cathelicidin (CATHL4 gene).
X67340
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9
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Matches:
Conservative:
Mismatches:
Indels:
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1. .550
                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                    4 LysTrpProTrpTrpProTrpArgArg 12
                                                                                                                                                                                                                                                                                                                                                                                   38 AAATGCCCGTGGTGGCCGTGGCGTCGT 64
                                                                                                                                                                                                                                                                                                                                        US-09-444-281-35 (1-13) x AR282754 (1-211)
              AR282754.1 GI:29719494
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100.00%
80.22%
                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
 AR282754
                                        Unknown.
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Pred. No.:
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           VERSION
KEYWORDS
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BTINDLCD
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AUTHORS
TITLE
JOURNAL
MEDLINE
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AUTHORS
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JOURNAL
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                          PAT 18-DEC-2003
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                                                                                                                                  1 (bases 1 to 69)
Wood, T. K., Jayaraman, A. and Earthman, J.C.
Inhibition of sulfate-reducing-bacteria-mediated degradation using
bacteria which secrete antimicrobials
Patent: US 6630197-A 1 07-OCT-2003;
Location/Qualifiers
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M Unknown.

JE (bases 1 to 211)

JE Selsted, M. E. and Osapay, K.

E Crosslink-stablized indolicidin analogs

ANAL Patent: US 6444645-A 11 03-SEP-2002;

ARES 1. -211

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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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Sequence 11 from patent US 6444645.
AR226388
                    Sequence 1 from patent US 6630197.
AR404925
AR404925.1 GI:40153719
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Sequence 38 from patent US 6524585.
                                                                                                                                                                                                                       1. .69
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                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LysTrpProTrpTrpProTrpArgArg 12
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Unclassified.
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Query Match:
                                                                                             Unknown.
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LOCUS DEFINITION ACCESSION

RESULT 8 AR226388

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ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

source

TITLE JOURNAL FEATURES

Pred. No.:

Score:

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LOCUS

RESULT 9 AR282754

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Query Match:

Pred. No.:

ORIGIN

MAM 15-NOV-2001

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AC146517.1 GI:34147313
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AC146517/c
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                                                                                           ORIGIN
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A process for isolating and purifying viruses, soluble proteins and
peptides from plant sources
                                                                                                                                                                                                                                                                                                                             PAT 17-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                           Unclassified.

1 (bases I to 6446)

2 (bases I to 6426)

3 (Adarger, 23.7, Holtz, R. Barry., McCulloch, M.J. and Turpen, T.H. Process for isolating and purifying viruses and sugars from plant
RVKQCVGTVTLDPSNDQFDLNCNELQSVILPWKWPWWRRG"
                                                                                                                                                                                                                                                                                                                             linear
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent: US 6303779-A 5 16-OCT-2001;
                                                                                                                                                                                                                                                                                                                        AR173324 6446 bp
Sequence 5 from patent US 6303779.
AR173324
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          13. .99
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403. .44
/gene="CATHL4"
/product="cathelicidin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX098418 6446 bp
Sequence 5 from Patent W00119969.
AX098418
                                                                                                                                                                                                                                                             415 AAATGGCCATGGTGGCCTTGGCGCAGA 441
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1. .6446
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                                                                                                                                      Score:
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ACL46517 156785 bp DNA linear HTG 24-AUG-2003
Homo sapiens chromosome 16 clone RP11-67B18, WORKING DRAFT
SRQUENCE, 15 unordered pieces.
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DIR Joint Genome Institute.

Direct Submission

Submitted (14.AUG-2003) Production Sequencing Facility, DOR Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA -----Genome Center

Center: Joint Genome Institute

Center: Gode: JGI
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DOB Joint Genome Institute.
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Consensus quality: 149669 bases at least Q30
Consensus quality: 150663 bases at least Q30
Estimated insert size: 175000; agarose-fp estimation
Betimated insert size: 15386; sum-of-contigs estimation
Quality coverage: 9.57 in Q20 bases; agarose-fp estimation.
Quality coverage: 10.77 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a "vorking draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1118: contig of 1118 bp in length
1128: gap of unknown length
2329: contig of 1111 bp in length
2429: gap of unknown length
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Homo sapiens (human)
Homo sapiens
                                                                                        1. 6446
/organism="Nicotiana benthamiana"
/mol_type="unassigned RNA"
/db_xref="taxon:4100"
                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Patent: WO 0119969-A 5 22-MAR-2001;
Large Scale Biology Corporation (US)
Location/Qualifiers
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Unpublished
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Center clone name: RPCI-11_67B18
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Direct Submission

Submitted (04-DEC-2002) DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Dec 4, 2002 this sequence version replaced gi:16041346.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos National Laboratory
www-sigo:stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Exrors is 0.2.
Location/Qualifiers
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Homo appiens chromosome 16 clone RPI1-715J22, complete sequence.
ACI06820
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94598, USA
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Submitted (02-JUL-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
5. (bases I to 176552)
Stanford Human Genome Center and Los Alamos National Laboratory.
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DOB Joint Genome Institute.

District Submission

Submitted (27-MAR-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
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On Nov 26, 2003 this sequence version replaced gi:21672112.
Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (12-JAN-2002) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walmut Creek, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                     157518
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
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/db_ref="texon:9606"
/chromosome="16"
/clone="RP11-20123"
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Unpublished
2 (bases 1 to 176552)
DOE Joint Genome Institute.
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DOE Joint Genome Institute.
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Direct Submission
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91.67%
83.33%
75.82%
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Best Local Similarity:
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JOURNAL
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Homo sapiens chromosome 16 clone RP11-20123, complete sequence.
ACO93525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submitted (11-AUG-2001) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 157518)
DOE Joint Genome Institute, Stanford Human Genome Center and Los Alamos National Laboratory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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DOE Joint Genome Institute, Stanford Human Genome Center and Los
Alamos National Laboratory.
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                                                                                                                                                                                                                                                                1. gap of unknown length
2. contig of 9113 bp in length
3. gap of unknown length
3. contig of 12880 bp in length
4. gap of unknown length
5. contig of 17790 bp in length
6. gap of unknown length
7. gap of unknown length
contig of 1138 bp in length gap of unknown length contig of 1049 bp in length contig of 1049 bp in length contig of 2996 bp in length gap of unknown length gap of unknown length contig of 4819 bp in length contig of 4819 bp in length contig of 4819 bp in length gap of unknown length contig of 4378 bp in length gap of unknown length gap of unknown length contig of 4378 bp in length gap of unknown length contig of 9378 bp in length gap of unknown length
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114256: gap of unknown length
57 156785: contig of 42529 bp in length.
Location/Qualifiers
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/clone="RP11-67B18"
/clone_lib="RPCI human BAC library 11"
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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DOE Joint Genome Institute.
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www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center and Los Alamos
National Laboratory
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.4.
S
1. 176552
Aurce /organism="Homo sapiens"
/mol_type="qqnomic DNA"
/db xref="taxon:9606"
/chromosome="16"
/chromosome="16"
/clone="RPH1-715522"
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Percent Similarity: 9
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Search completed: May 11, 2004, 16:01:29 Job time : 2429.08 secs

US-09-444-281-35 (1-13) x AC106820 (1-176552)

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Aad45350
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                                                   AAI 72481
AAZ40246
AAZ49764
AAZ45123
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ABL21537
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(KAYW/) KAY W W.
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Aax83788 Antimicro
Aaz29389 PCR prime
Aaz29330 PCR prime
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                                                                                     May 11, 2004, 12:39:07; Search time 256.88 Seconds (without alignments) 214.990 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                        6747726
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                               nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                            3373863 seqs, 2124099041 residues
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Listing first 45 summaries
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Database :

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Minimum DB s Maximum DB s

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alp GPC Blr Blr

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This oligonucleotide was used as a template in a PCR reaction (see also AAV6099-10) to generate a DNA fragment encoding the cationic peptide MBILI (see AAW1690). The PCR product was cloned into the universal vector pR2h-BI, which contains the R21 replication leader of RepA (see AAW71696) and 2 tandem copies of the prepro region (Hpro) of human defensin. The vector provides expression of R21-hpro-MBILI funsion in host cells. The invention provides controlled replication plasmid vectors (RAMP vectors) comprising a replication origin of a small cryptic plasmid such as pKLI (see AAV58292) and a gene encoding RepA (see AAW71666). The vectors can reach very high levels of plasmid replication, but are not lethal to the host cell, and can be used to direct the high level expression of e.g. cytokines, antigens and therapeutic proteins
small cryptic plasmid ori sequence, useful for high level expression e.g. cytokines, antigens or therapeutic proteins.
                                                                                     Example 16; Page 57; 82pp; English
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Sequence 88 BP; 20 A; 18 C; 25 G; 25 T; 0 U; 0 Other;

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              Matches:
Conservative:
Mismatches:
Indels:
             91.00
100.00%
100.00%
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                      Percent Similarity:
Best Local Similarity:
Alignment Scores:
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US-09-444-281-35 (1-13) x AAV60908 (1-88)

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| IleLeuLysLysTrpProTrpTrpProTrpArgLys
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BP.

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AAA27291 standard; DNA; 114
             (first entry)
            20-SEP-2000
        AAA27291;
RESULT 2
  AAA27291
      \mathbb{Z}
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Oligonucleotide used for synthesis of MBI-11 fragment

Oligonucleotide; cellulose binding domain; CBD; cationic peptide; MBI-11; indolicidin; bovine; ss.

Synthetic.

WO200031279-A2.

02-JJN-2000

99WO-CA001107. 19-NOV-1999; 98US-0109218P 20-NOV-1998;

(MICR-) MICROLOGIX BIOTECH INC.

Bartfeld D; Burian J,

WPI; 2000-400086/34.

Multi-domain fusion protein expression cassette used for high yield

stable production of foreign peptide gene products.

A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-domain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the Example 4; Page 37; 73pp; English.

Sequence 108 BP; 18 A; 33 C; 31 G; 26 T; 0 U; 0 Other;

Alignment Scores:

fragment was used in the expression cassette. MBI-peptide derived from modifications of indolicidin

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positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This cassette allows high yield, stable production of the cationic peptide. Cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an obligonucleotide that was used to synthesise a MBI-II fragment. MBI-II is a cationic peptide derived from modifications of indolicidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-domain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of anionic peptide expressed as an insoluble protein. The inclusion of anionic peptide sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion of the cationic peptide allows high yield, stable production of the cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligomucleoride that was used to synthesise a MBI-11B7 fragment. This fragment was used in the expression cassette. MBI-11B7 is a cationic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide, cellulose binding domain, CBD, cationic peptide; MBI-11; indolicidin; bovine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multi-domain fusion protein expression cassette used for high yield stable production of foreign peptide gene products.
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                                                                                                                               Sequence 114 BP; 25 A; 26 C; 30 G; 33 T; 0 U; 0 Other;
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Query Match: DB:

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Pred. No.:

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A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multidomain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of anionic peptide expressed as an insoluble protein. The inclusion of approte in sequences in the linker sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This casette allows high yield, stable production of the cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligonucleotide that was used in the expression cassette. MBI-11B7 fragment. This fragment was used in the expression cassette. MBI-11B7 is a cationic peptide derived from modifications of indolicidin
                                                                                                                                                                                                                                                                          Oligonuclectide; cellulose binding domain; CBD; cationic peptide; MBI-11; indolicidin; bovine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multi-domain fusion protein expression cassette used for high yield stable production of foreign peptide gene products.
                                                                                                                                                                                                                                    Oligonucleotide used for synthesis of MBI 2X11B7 last cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 151 BP; 22 A; 44 C; 49 G; 36 T; 0 U; 0 Other
AIGATTCTGCGTTGGCCGTGGTGGCCGTGGCGTAA B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 AIGATTCTGCGTTGGCCGTGGTGGCCGTGGCCGTCGCAAA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IleLeuLysLysTrpProTrpProTrpArgArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-444-281-35 (1-13) x AAA27294 (1-151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Page 38; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                           AAA27294 standard; DNA; 151 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-CA001107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0109218P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 39
                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.36
76.00
92.31%
69.23%
83.52%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burian J, Bartfeld D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-400086/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                        WO200031279-A2.
                                                                                                                                                                                              20-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUN-2000.
                                                                                                                                                                                                                                                                                                                                              Synthetic.
                          44
                                                                                                                                                      AAA27294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
                                                                   RESULT
                                                                                                                                                        A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multidomain fusion protein expression cassette comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of positive charge of the cationic peptide sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion of the cationic peptide so that the charge of the fusion of the cationic peptides. Cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligomucleotide that was used to synthesise a MBI-11B7 fragment. This fragment was used in the expression cassette. MBI-11B7 is a cationic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cellulose binding domain; CBD; cationic peptide; MBI-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multi-domain fusion protein expression cassette used for high yield stable production of foreign peptide gene products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide used for synthesis of MBI 11B7 first cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 114 BP; 20 A; 34 C; 32 G; 28 T; 0 U; 0 Other;
                                                                                                                                                                                                                       38 ATGATICTGCGTTGGCCGTGGCCGTGGCGTCGCAAA 76
                                                                                                                                                                                            1 IleLeuLysLysTrpProTrpTrpProTrpArgArgLys 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide derived from modifications of indolicidin
Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                    US-09-444-281-35 (1-13) x AAA27296 (1-108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 40; 73pp; English.
                                                                                                                                                                                                                                                                                                                       AAA27298 standard; DNA; 114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MICR-) MICROLOGIX BIOTECH INC
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76.00
92.31%
69.23%
83.52%
  0.251
76.00
92.31%
69.23%
83.52%
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      indolicidin; bovine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bartfeld D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-400086/34.
                                          Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide;
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02-JUN-2000

Burian J,

Synthetic.

AAA27298;

AAA27298 RESULT g

151 9 1 0 0 0 0

Length:
Matches:
Conservative:
Mismatches:
Indels:

13

19-MAR-1999 (first entry)

1 IleLeuLysLysTrpProTrpTrpProTrpArgArgLys 13

à

US-09-444-281-35 (1-13) x AAA27298 (1-114)

Query Match:

Pred. No.:

AAV83788;

(first entry)

Synthetic.

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New DNA constructs useful for mass production of antimicrobial peptides
                                                                                                                  PCR primer-15 for synthesis of antimicrobial peptide Indolicidin gene.
                                                                                                                                                    PCR primer; anti-microbial peptide; Indolicidin gene; DNA construct; glutamine pyrophosphoribosyl pyrophosphate amidotransferase gene; purP gene; fusion peptide; mass production; pharmaceutical industry; food industry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim JH, Kang MH, Lee J, Park SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 13; 67pp; English.
AAZ29389 standard; DNA; 47 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAMY-) SAMYANG GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in microorganism hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-097542/08.
                                                                                                                                                                                                                                                                                                       WO9964611-A1.
                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1999;
                                                                              29-FEB-2000
                                                                                                                                                                                                                                                                                                                                               16-DEC-1999.
                                                                                                                                                                                                                                                                 Synthetic.
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  The invention relates to mass production of antimicrobial peptides. The method comprises constructing a fusion gene containing a first gene encoding a negatively charged acidic peptide having at least two cysteine residues, and a second gene encoding a positively charged basic antimicrobial peptide. A host microorganism is transformed with a vector containing the fusion gene and then cultured. The expressed antimicrobial peptides in recomminant microorganisms. The inhibitory effect of the expressed antimicrobial peptides in recomminant microorganisms. The inhibitory effect of the expressed antimicrobial peptide upon the growth of the host microorganism is considerably reduced by fusing it to the acidic peptide. Therefore, the use of the fusion gene provides an economic, recombinant alternative of mass produciny and poor economy, previoually encountered by recombinant and chemical methods. The present sequence represents the DNA encoding an antimicrobial peptide Indolicidin. This can be used along with the acidic peptide Guamerin gene in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New method for mass production of antimicrobial peptides - by constructing fusion genes comprising acidic and antimicrobial peptide genes and transforming host with vector containing these.
                                                                                                                                                                                                       1. .39 /*tag=\ a /*tag= a /note= "the start and stop codons are not indicated"
                                                           Antimicrobial; fusion; acidic peptide; recombinant; microorganism; guamerin; basic peptide; Indolicidin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39 BP; 4 A; 10 C; 16 G; 9 T; 0 U; 0 Other;
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Conservative:
Mismatches:
                     Antimicrobial peptide Indolicidin encoding DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SAMY-) SAMYANG GENEX CORP. (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-444-281-35 (1-13) x AAV83788 (1-39)
                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 6; Page 18; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       construction of the fusion gene
                                                                                                                                                                                                                                                                                                                                                                       98WO-KR000132.
                                                                                                                                                                                                                                                                                                                                                                                                             97KR-00021312
                                                                                                                                                                                                                                                                                                                                                                                                                                98KR-00013372
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73.00
100.00%
100.00%
80.22%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                      WO9854336-A1
                                                                                                                                                                                                                                                                                                                                                                       28-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                             28-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1998;
                                                                                                                                                                                                                                                                                                                              03-DEC-1998
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Kim S,

The

Lee

Hong SS,

Lee JW,

98KR-00022117. 99KR-00017920. 99WO-KR000282

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The present sequence is a chemically synthesised PCR primer which was used to synthesise a gene encoding antimicrobial peptide Indolicidin. antimicrobial peptide gene is used in a DNA construct that comprises entire, partial or a derivative of purF gene (glutamine pyrophosphoribosyl pyrophosphate amidotransferase gene). The DNA construct allows mass production of the antimicrobial peptide in microbial bests without killing the host cells. The antimicrobial peptides are useful commercially in the pharmaceutical and food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR primer-16 for synthesis of antimicrobial peptide Indolicidin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR primer, anti-microbial peptide, Indolicidin gene; DNA construct; glutamine pyrophosphoribosyl pyrophosphate amidotransferase gene;
                                                                                                                                                                                                               Sequence 47 BP; 6 A; 11 C; 19 G; 11 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 AAATGGCCGTGGTGGCCGTGGCGTCGT 43
                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-444-281-35 (1-13) x AAZ29389 (1-47)
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100.00%
80.22%
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Best Local Similarity:
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                                                                                                                                                                                  industries
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DB:
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ID AAZ293
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RESULT 7

셤

Query Match: DB:

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Disclosure; Page 7; 56pp; Korean.
(SAMY-) SAMYANG GENEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                       ABL60415;
                  Hong SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hong SS,
                                                                                                                                                                                                                                                                                     Query Match:
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ò
                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is a chemically synthesised PCR primer which was used to synthesise a gene encoding antimicrobial peptide Indolicidin. The antimicrobial peptide gene is used in a DNA construct that comprises entire, partial or a derivative of purf gene (glutamine pyrophosphoribosyl pyrophosphate amidotransferase gene). The DNA construct allows mass production of the antimicrobial peptide in microbial hosts without killing the host cells. The antimicrobial peptides are useful commercially in the pharmaceutical and food
                                                                                                                                                                              New DNA constructs useful for mass production of antimicrobial peptides
purF gene; fusion peptide; mass production; pharmaceutical industry;
food industry; ss.
                                                                                                                                            Lee H;
                                                                                                                                            Hong SS,
                                                                                                                                                                                                                                                                                                               G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           400000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene expression; peptide antibiotic; purF gene; ds.
                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                            Lee JW,
                                                                                                                                                                                                                                                                                                                                                                                                                           LysTrpProTrpTrpProTrpArgArg 12
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAATGGCCGTGGTGGCCGTGGCGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                        US-09-444-281-35 (1-13) x AAZ29390 (1-47)
                                                                                                                                            Kim JH, Kang MH, Lee J, Park SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA fragment of the invention #15.
                                                                                                                                                                                                         Example 1; Page 13; 67pp; English.
                                                                                                                                                                                                                                                                                                                 Sequence 47 BP; 12 A; 18 C; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL60414 standard; DNA; 47 BP
                                                                              99WO-KR000282.
                                                                                               98KR-00022117.
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                                                                                                                                                                                                                                                                                                                                           0.235
73.00
100.00%
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                                                                                                                         (SAMY-) SAMYANG GENEX CORP.
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                                                                                                                                                                                       in microorganism hosts.
                                                                                                                                                            WPI; 2000-097542/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
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                                                                              08-JUN-1999;
                                                                                                       14-MAY-1999;
                                            WO9964611-A1
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                                                             16-DEC-1999.
                                                                                                                                                                                                                                                                                                industries
                           Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
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antibiotics effectively from microorganisms. The generic component consists of a first gene sequence which codes for the whole or partial purf gene or its derivative, and a second gene sequence which codes peptide antibiotics. The mass-production method of peptide antibiotics comprises the steps of, constructing an expression vector including the genetic component, transforming a bacterial host cell with the vector, culturing the transformed cell to express the genetic component reasonable from the group consisting of pGNX2, pGNX3, pGNX4 and pGNX5, and it has a high copy number of crigin, strong transcription promoter and structural gene. The sequences given in records ABL60460-ABL60464 represent DNA sequences of the invention
                                                                                       Gene expression system useful for mass-production of peptide antibiotics and vectors derived from microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene expression system useful for mass-production of peptide antibiotics and vectors derived from microorganisms.
                                                                                                                                                                                                             invention relates to a genetic component which mass-produces peptide
SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Park SH;
Park
Lee JW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 47 BP; 6 A; 11 C; 19 G; 11 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
  Lee JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee JH,
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Lee HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 AAAregccereereecereecereer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-444-281-35 (1-13) x ABL60414 (1-47)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA fragment of the invention #16.
                                                                                                                                                                   Disclosure; Page 7; 56pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL60415 standard; DNA; 47 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-2001; 2001KR-00031889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUN-2001; 2001KR-00031889
  Kang MH, Kim JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim JH,
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73.00
100.00%
100.00%
80.22%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-301977/34.
                                               WPI; 2002-301977/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity:
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Claim 1; Fig 1; 67pp; English.

The invention relates to a genetic component which mass-produces peptide antibiotics effectively from microorganisms. The genetic component consists of a first gene sequence which codes for the whole or partial purf gene or its derivative, and a second gene sequence which codes peptide antibiotics. The mass-production method of peptide antibiotics component, transforming a bacterial host cell with the vector, colluting the transformed cell to express the genetic component, and recovering the peptide antibiotics. The expression vector is selected from the group consisting of policy, The expression vector is selected from the group consisting of policy transcription promoter and structural gene. The sequences given in records ABL60400-ABL60464 represent DNA sequences of the invention

Sequence 47 BP; 12 A; 18 C; 10 G; 7 T; 0 U; 0 Other;

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      Length:
Matches:
Conservative:
Mismatches:
                                         Indels:
       0.235
73.00
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80.22%
                        Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
                                        Query Match:
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US-09-444-281-35 (1-13) x ABL60415 (1-47)

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4 LysTrpProTrpTrpProTrpArgArg 12
            35 AAATGGCCGTGGTGGCCGTGGCGT 9
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AAZ29364 standard; DNA; 53 (first entry) 29-FEB-2000 AAZ29364; RESULT 11 AAZ29364 a

Antimicrobial peptide, Indolicidin encoding DNA.

purF gene; glutamine pyrophosphoribosyl pyrophosphate amidotransferase; purF derivative; fusion partner; antimicrobial peptide; Indolicidin; mass production; cleavage site; hydroxylamine; CNBr; DNA construct; cow; neutralise; toxicity; pharmaceutical industry; food industry; ds.

Bos taurus

/*tag= a /product= "Indolicidin peptide" /note= "Antimicrobial peptide used in DNA construct" Location/Qualifiers

W09964611-A1

16-DEC-1999

99WO-KR000282. 08-JUN-1999; 98KR-00022117. 99KR-00017920. 09-JUN-1998; 14-MAY-1999;

SAMY-) SAMYANG GENEX CORP.

Lee H; Hong SS, Lee JW, Lee J, Park SH, Kang MH, Kim JH,

WPI; 2000-097542/08. P-PSDB; AAY44324. New DNA constructs useful for mass production of antimicrobial peptides in microorganism hosts.

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The present DNA sequence encodes an antimicrobial peptide, Indolicidin derived from cow, Bos taurus. It is used along with a derivative of purf gene sequence that functions as a fusion partner. A DNA construct that comprises, this antimicrobial peptide encoding sequence and the entire, partial or derivative of purf gene, is used for mass production of the antimicrobial peptide in microorganisms without killing the host cells. Use of the purf gene derivative sequence, neutralises the toxicity of the antimicrobial peptides against the host microorganism. The antimicrobial peptides are useful commercially in the pharmaceutical and food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a genetic component which mass-produces peptide antibiotics effectively from microorganisms. The genetic component consists of a first gene sequence which codes for the whole or partial purF gene or its derivative, and a second gene sequence which codes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene expression system useful for mass-production of peptide antibiotics
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                                                                                                                                                                       Sequence 53 BP; 8 A; 12 C; 20 G; 13 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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partial
note= "no start codon present"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and vectors derived from microorganisms.
                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                        12
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                                                                                                                                                                                                                                                                                                                                        4 LysTrpProTrpTrpProTrpArgArg
                                                                                                                                                                                                                                                                                                           US-09-444-281-35 (1-13) x AAZ29364 (1-53)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA fragment of the invention #44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Page 17; 56pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-JUN-2001; 2001KR-00031889
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100.00%
80.22%
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                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KR2001098973-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                     Alignment Scores:
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                                                                                                                                                  industries
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL60445;
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peptide antibiotics. The mass-production method of peptide antibiotics comprises the steps of; constructing an expression vector including the genetic component, transforming a bacterial host cell with the vector, culturing the transformed cell to express the genetic component, and recovering the peptide antibiotics. The expression vector is selected from the group consisting of pGNX2, pGNX3, pGNX4 and pGNX5, and it has a high copy number of origin, strong transcription promoter and structural gene. The sequences given in records ABL60400-ABL60464 represent DNA sequences of the invention
            88888888888
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Sequence 53 BP; 8 A; 12 C; 20 G; 13 T; 0 U; 0 Other;

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      Length:
Matches:
Conservative:
Mismatches:
                                      Indels:
      0.267
73.00
100.00%
100.00%
80.22%
                            Best Local Similarity:
Query Match:
DB:
                      Percent Similarity:
Alignment Scores:
        ..
No.:
         Pred
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US-09-444-281-35 (1-13) x ABL60445 (1-53)

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cDNA derived from C-terminus of ubiquitin.
                17 AAATGGCCGTGGTGGCCGTGGT 43
LysTrpProTrpTrpProTrpArgArg 12
                                                                                            AAI72481 standard; cDNA; 68
                                                                                                                                                      (first entry)
                                                                                                                                                      16-MAY-2002
                                                                                                                         AAI72481;
                                                           RESULT 13
                                                                             AAI 72481
                              q
 à
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Recursive ensemble mutagenesis; REM; cell viability; optical signal; high-throughput screening; antimicrobial compound; antibiotic; ss. .30, aa:Trp /transl_except= pos:28. .30, a /note= "No start codon given" Location/Qualifiers /*tag= a /partial 9. Synthetic. Key

WO200206517-A2.

24-JAN-2002.

19-JUL-2001; 2001WO-US023004.

19-JUL-2000; 2000US-0219179P.

(KAIR-) KAIROS SCI INC.

Bylina EJ, Coleman WJ, WPI; 2002-179801/23. P-PSDB; AAB47907

Youvan DC;

Screening compounds affecting cell viability e.g. for identifying antimicrobial compounds, comprises determining if induced transformed cell colonies have a desired signal when contacted with a viability indicator.

Disclosure; Fig 6; 56pp; English.

This sequence is derived from the C-terminus of ubiquitin and represents the cloning region. SacII-BglII cassettes can be used for inserting antimicrobial peptide sequences into this region. This sequence may be

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used to form the recursive ensemble mutagenesis (REW) cassette of the invention. The cassette may be used in the method of the invention for determining whether a compound affects cell viability by: (a) exposing colonies of cells (CC) on a support surface to inducing conditions, where the cells have been transformed with an expression library encoding candidate compounds; (b) contacting CC with a viability indicator that produces an optical signal indicative of cell viability indicator that produces an optical signal indicative of cell viability, and (c) determining is a colony has a desired optical signal. The method is useful for high-throughput screening to identify antimicrobial compounds and in drug discovery. The antimicrobial compounds are useful in the paramaceutical industry, and provide an additional new class of pharmaceutical industry, and provide an additional new class of continionation of the authentic peptide sequences contained in an expression library for antimicrobial activity, for distinguishing dead cells (expressing active sequences) from living cells (expressing inactive or less active sequences) to identify novel antimicrobial peptide sequences, including highly potent molecules, resulting in a large number of new antimicrobial lead compounds that are active against a broad range of new antimicrobial lead compounds are active against a broad range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of bacteria or other microorganisms, and for screening all types of antibiotic compounds, including libraries of low molecular weight molecules produced by metabolic engineering and artificial synthesized libraries in solid-phase arrays
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Sequence 68 BP; 11 A; 18 C; 19 G; 20 T; 0 U; 0 Other;

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Conservative:
Mismatches:
Indels:
       Length:
Matches:
       0.349
73.00
100.00%
100.00%
80.22%
                                        Best Local Similarity:
                              Percent Similarity:
Alignment Scores:
                                                  Query Match:
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US-09-444-281-35 (1-13) x AAI72481 (1-68)

4 LysTrpProTrpTrpProTrpArgArg 12

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AAZ40246 standard; DNA; 69 BP. RESULT 14 AAZ40246 ß

AAZ40246;

(first entry) 23-FEB-2000 Oligonucleotide for cloning indolicidin peptide coding sequence

Indolicidin; bactenecin; sulphate-reducing bacteria; growth inhibitor; corrosion; degradation; metal; concrete; cement; dental implant; biofilm;

Synthetic. Bacillus sp.

W09956553-A1

99WO-US009675. 03-MAY-1999;

11-NOV-11999

99US-00282277. 98US-00074037 06-MAY-1998; 31-MAR-1999;

(REGC) UNIV CALIFORNIA.

Earthman JC; Wood TK, Jayaraman A,

WPI; 2000-052882/04.

Inhibiting growth of sulfate-reducing bacteria using other bacteria,

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particularly for protection of metals and concrete.
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This sequence represents an oligonucleotide for cloning the non-amidated indolicidin peptide coding sequence. The invention relates to a method condicidin peptide coding sequence. The invention relates to a method controlicidin peptide coding sequence. The invention relates to a method correct for inhibiting growth of sulphate-reducing bacteria (A) on a material (B) sensitive to corrorsion or degradation, but of the particular or correct or care to sensitive to correct or care to gainst corrosion and degradation, but (B) can also be used to protect dental implants. (B) is present in an open or closed system (e.g. water cooling tower, liquid storage container, fuel tank, sewer or drainage system etc.) or part of a cridge or other structure. The method is more effective and less capensive than known methods for inhibiting (A), and reduces the amount of toxic chemicals released. Conventional biofilms of acrobic organisms of toxic chemicals released. Conventional biofilms of acrobic organisms or produced exactly where they are required and inhibit (A) without correstance of (A) to conventional biocides, which may then be used in reduced amounts). If local damage to the biofilm occurs, the underlying correstance is still protected by diffusion of (I) from neighbouring areas
Example 4; Fig 1; 84pp; English
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Sequence 69 BP; 14 A; 18 C; 20 G; 17 T; 0 U; 0 Other;

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Length:
Matches:
Conservative:
Mismatches:
                                                         Indels:
                                                                                                                       4 LysTrpProTrpTrpProTrpArgArg 12
                                                                                             JS-09-444-281-35 (1-13) x AAZ40246 (1-69)
                               100.00%
100.00%
80.22%
         0.355
                                               Local Similarity:
                                    Percent Similarity:
Alignment Scores:
                                                           Query Match:
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Poly-(Indol (1-13)-Met-Ala-Arg-Ile-Ala-Met)3 DNA. 28 AAATGGCCTTGGTGGCCTTGGCGCGC 54 AAZ49764 standard; DNA; 211 BP. (first entry) 18-APR-2000 RESULT 15 AAZ49764 a

crosslinked indolicidin analog; X-indolicidin; poly-Indol 1-13; stability; bovine neutrophil; antimicrobial; antibacterial; fungicide; protozoacide; virucide; anti-HIV; human immunodeficiency virus-1; HIV-1; gram positive bacteria; gram negative; Staphylococcus auteus. Becherichia coli; Salmonella typhimurium; yeast; fungi; protozoa; candida albicans; Cryptococcus neoformans; Giardia; Acanthamoeba; hexapeptide spacer; ds.

Location/Qualifiers 1. .199 *tag= a 1. .21 /*tag= primer_bind Synthetic. Bos sp.

Q

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/*tag= d
/note= "corresponds to overlap in oligonucleotides used
for ligation"
/product= "Poly-(Indol(1-13)-Met-Ala-Arg-Ile-Ala-Met)3"
/note= "encodes three copies of Indol 1-13, each
separated by Met-Ala-Arg-Ile-Ala-Met spacer sequence"
                                                                                                                 misc_feature
```

The patent discloses crosslinked analogs of indolicidin (Indol 1-13)

which is a naturally occurring peptide isolated from bovine neutrophils

which is a naturally occurring peptide isolated from bovine neutrophils

and has antimicrobial activity. The crosslinked indolicidin (Xindolicidin) analogs are stable and have antimicrobial activity against

cyam positive and negative bacteria (e.g. Staphylococcus aureus,

gram positive and negative bacteria (e.g. Staphylococcus aureus,

cyam positive and negative bacteria (e.g. Staphylococcus aureus,

commissing a surformane), protozoa (e.g. diardia

cyam beat borana continition the growth or survival of microorganisms

cused for reducing or inhibiting the growth or survival of microcoganisms

cused for reducing a surface, or a mammal. The present sequence is a DNA

cencoding a protein comprising three copies of Indol 1-13 each separated

by a hexapeptide spacer sequence. The sequence was used to produce a

comprising comprising three copies of Indol 1-13 each separated

by a hexapeptide spacer sequence. The sequence was used to produce a

concominant construct for the expression of Indol-homoserine (Hse)

carivity provides a means to produce X-indolicidin analog precursors in

cyampic of the sequence X-indolicidin analog precursors in

cyampic of the sequence X-indolicidin analog recorsing the sequence X-indolicidin analog mannal and X-indolicidin analog mannal A-indolicidin analo 148. .151 /*tag= e /note= "corresponds to overlap in oligonucleotides used Crosslinked indolicidin analogs with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses. Sequence 211 BP; 36 A; 50 C; 74 G; 51 T; 0 U; 0 Other; 211 9 0 0 0 0 Length:
Matches:
Conservative:
Mismatches: for ligation" complement (191. .211) /*tag= c Example 1C; Fig 1; 53pp; English. 99WO-US011165. 98US-00099631. 1.18 (REGC) UNIV CALIFORNIA. Osapay K; WPI; 2000-147133/13. P-PSDB; AAY44668. Alignment Scores: 20-MAY-1999; 18-JUN-1998; W09965510-A1 misc_feature 23-DEC-1999, Selsted ME, primer_bind

4 LysTrpProTrpTrpProTrpArgArg 12 US-09-444-281-35 (1-13) x AAZ49764 (1-211) 38 AAATGGCCGTGGTGGCCGTGGCGTCGT

Indels:

100.00% 100.00% 80.22%

Percent Similarity: Best Local Similarity:

Query Match

Gaps:

Search completed: May 11, 2004, 14:43:51 Job time : 260.88 sec8

1402, Ap 1394, Ap 1, Appli 1, Appli

Sequence

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OM protein

Run on:

Sequence:

Searched:

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APPLICANT: Burian, Jan
APPLICANT: KAY, William W.

TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM
TITLE OF INVENTION: SMALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING
TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
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COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,071
FILING DATE: 13-MAR-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCMASTERS, David D.
REGISTRATION NUMBER: 33,963
REGISTRATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: COMPANATION INFORMATION:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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6300 Columbia Center, 701 Fifth Avenue
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PCT-US95-05467-1
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US-09-023-655-1402
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US-09-395-115-1
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US-09-632-098-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-09-042-071-49
    Command line parameters:
-MODEL=frame+ p2n.model -DEW=x1h
-Q=/cgn2 1/USPTO_gpool/USO3442281/runat 07052004 171139 2589/app_query.fasta_1.398
-Q=/cgn2 1/USPTO_gpool/USO3442281/runat 07052004 171139 2589/app_query.fasta_1.398
-Q=/cgn2 1/USPTO_gpool/USP24281/runat 070FIX=x10 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=blits -STRXT=1 -END=-1 -MATRIX=blosum62 -TRANS=humman40.cdi
-LIST=45 -DCOALIGN=200 -THR SCORE-pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-UNITS=51ts -OOTENT=-pto -NORM=ext - THR MAX=100 -THR MIN=0 -ALIGN=15
-USFR=USO3444281 @CGN 1 1 76 @runat 07052004 171139 2589 -NCPD=6 -ICPU=3
-NO MAAD -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-PBW TINBOJT=120 -WARN ITMEOUT=30 - THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELCP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11, Appl
38, Appl
5, Appli
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5, Appli
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9298, Ap
9281, Ap
1, Appli
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Sequence 29, Appl
Sequence 1, Appli
                                                                                                                                                                      (without alignments)
144.518 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 3
Sequence 5
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                                                                                                                                                May 11, 2004, 14:02:47; Search time 49.92 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_comB.seq:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                        - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-9269
US-09-252-991A-9298
US-09-252-991A-9281
US-08-159-784-1
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US-09-230-180-29
US-09-282-277-1
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US-09-416-481A-38
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US-09-037-751-5
US-09-466-422-5
                                                                                                                                                                                                                                                                                                                                                                                                                                              682709 seqs, 277475446 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                  BLOSUM62
Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                   US-09-444-281-35
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Match Length
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73
73
73
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60
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Result No.

26430701110

Sequence 57, Appl

Sequence

Sequence

Sequence

Sequence

Sequence

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FATERLE WO. 6.10.39.94.

GENERAL INFORMATION:
APPLICANT: Kim, Sun-Chang
APPLICANT: Lee, Jae Hyun
APPLICANT: Kim, Jeon-Chang
APPLICANT: Kim, Jeon-Chang
APPLICANT: Kim, Jeong Hyun
APPLICANT: Kim, Jeong Hyun
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
APPLICANT: Scanged Ministre of Science and Technology
ITILE OF INVENTION: MATHOD FOR MASS PRODUCTION OF
ITILE OF INVENTION: ANTIMICROBIAL PEPTIDE
ITILE OF INVENTION: ANTIMICROBIAL PEPTIDE
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDE
TITLE OF INVENTION NUMBER: PG(99/230,180)
CURRENT FILING DATE: 1999-03-10
PRIOR PELING DATE: 1998-04-09
PRIOR PELING DATE: 1998-04-09
PRIOR PELING DATE: 1998-04-09
PRIOR PELING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: DNA sequence deduced from Indolicidin peptide; CTHER INFORMATION: sequence based on codon usage of E. coli US-09-230-180-29
                                                                                                                                      88
0 0 0 0
                                                                                                                                                                                                                                                                                                                1 lieLeulyslysTrpProTrpTrpProTrpArgArgLys 13
                                                                                                                                                                                                                                                                                                                                         25 ATCCTGAAAAATGGCCGTGGTGGCCGTGGCGTCGTAAA 63
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                         US-09-444-281-35 (1-13) x US-09-042-071-49 (1-88)
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                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 29, Application US/09230180
; Patent No. 6183992
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US-092-282-277-1
'Sequence 1, Application US/09282277
'Fatent No. 6630197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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88 base pairs
                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                Best Local Similarity:
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                                                                            US-09-042-071-49
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DB:
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Query Match:
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APPLICANT: Wood, Thomas K.
APPLICANT: Wood, Thomas K.
APPLICANT: Wood, Thomas K.
APPLICANT: Barthman, James C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Inhibition of Sulfate-Reducing-Bacteria-Mediated
TITLE OF INVENTION: Inhibition of Sulfate-Reducing-Bacteria-Mediated
TITLE OF INVENTION: Inhibition Of Sulfate-Reducing-Bacteria-Mediated
TITLE OF INVENTION: Degradation Using Bacteria Which Secrete Antimicrobials
FILE REPERENCE: 02307E-085910US
CURRENT PILING DATE: 1999-03-31
EARLIER TIING DATE: 1999-03-31
EARLIER TIING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide; OTHER INFORMATION: used for cloning indolicidin
US-09-282-277-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (8)...(196)
OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-099-631A-11

Sequence 11, Application US/0909631A

Patent No. 644645

GREERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Selsted, Michael E.

APPLICANT: Geapay, Klara

TITLE OF INVENTION: Crosslink-Stabilized Indolicidin Analogs

FILE REFERENCE: P-UC 3050

CURRENT APPLICATION NUMBER: US/09/099,631A

CURRENT FILING DATE: 1998-06-18

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.1
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Best Local Similarity:
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Best Local Similarity:
Query Match:
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SEQ ID NO 11
LENGTH: 211
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TELEX:
INFORMATION FOR SEQ ID NO:
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09259741
Patent No. 6033895
GENERAL INFORMATION:
APPLICANT: GARGER, STEPHEN
APPLICANT: MCCULLOCH, MICHAEL
APPLICANT: MCCULLOCH, MICHAEL
APPLICANT: TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
TITLE OF INVENTION: PURIPYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT
TITLE OF INVENTION: SOURCES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWEVEY & SIMON
STREET: 1229 Pennsylvania Avenue N.W.
                                                                ; Sequence 38, Application US/09416481A; Sequence 38, Application US/09416481A; Sequence 38, Application US/09416481A; Patent No. 6524585; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael B.; TITLE OF INVENTION: Indolicidin Analogs and Methods of Using Same; FILE REFERENCE: P-UC 3794
; CURRENT APPLICATION NUMBER: US/09/416,481A; CURRENT RILING DATE: 1998-10-12; PRIOR RILING DATE: 1998-05-12; PRIOR FILING DATE: 1998-05-12; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYER. DISABLE FORM:
MEDIUM TYER. DISABLE COMPACTION
COMPUTER: IBM COMPACTION
OPERATING SYSTEM: DOS
SOFTWARE: FRASESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/259,741
FILING DATE: February 25, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-444-281-35 (1-13) x US-09-416-481A-38 (1-211)
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38 AAATGGCCGTGGTGGCCGTGGCGTCGT 64
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APPLICATION NUMBER: 09/037,751
                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (8)..(196)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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                                                             US-09-416-481A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-416-481A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
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US-09-259-741-5
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GENERAL INCORMATION:
APPLICANT: HOLTZ, K. BARRY
APPLICANT: HOLTZ, K. BARRY
APPLICANT: HOLTZ, K. BARRY
APPLICANT: HOLTZ, K. BARRY
APPLICANT: HOLTZ, M. CHAEL
APPLICANT: TURPEN, THOMAS
ITILE OF INVENTION: PROM PLANT SOURCES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEB: HOWITEY & Simon
STREET: 1299 Pennsylvania Avenue N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAID.

COMPUTER: USA
ZIP: 20004
ZIP: 20004
COMPUTER: Disket:
MEDIAN TYPE: Disket:
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: ASSTEM: DOS
SOFTWARR: PastSEM COM Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,751
                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
FILING DATE: March 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P
REGISTRATION UNMER: 25,277
REFERENCE/DOCKET NUMBER: 00801.0140.US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8100
TELEFAX: 650-463-8400
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-444-281-35 (1-13) x US-09-259-741-5 (1-6446)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET VIMBER: 0080
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 6446 base pairs TYPE: nucleic acid STRANDENNESS: single TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: Genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                 17.2
73.00
100.00%
100.00%
80.22%
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Sequence 9269, Application US/09252991A
Patent No. 6551795
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US-09-252-991A-9269
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 TrpProTrpTrpProTrpArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9269
LENGTH: 1278
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63.00
100.00%
100.00%
17.2
73.00
100.00%
100.00%
80.22%
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Best Local Similarity:
Query Match:
                                  Percent Similarity:
Best Local Similarity:
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US-09-252-991A-9298/c
                                                                                                                                                                                                                                                       US-09-252-991A-9269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                      Query Match:
 Pred. No.:
                                                                                                                                                                                                  셤
                                                                                                                                                                 ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: A PROCESS FOR ISOLATING AND PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT SOURCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/466,422
FILING DATE: 17-Dec-1999
CLASSIFICATION: UNMER: 09/037,751
APPLICATION NUMBER: 09/037,751
FILING DATE: CLIKNOWN:
APPLICATION NUMBER: 09/037,751
FILING DATE: CLIKNOWN:
APPLICATION NUMBER: 09/037,751
FILING DATE: CLIKNOWN:
APPLICATION NUMBER: 09/037,751
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 25,277
TELEPOWNICATION INFORMATION:
TELEPRAN: 650-463-8400
                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1299 Pennsylvania Avenue N.W. CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                             US-09-444-281-35 (1-13) x US-09-037-751-5 (1-6446)
                                                                                                                                                                                                                                                                                                                                                      6213 AAGUGGCCUUGGUGGCCAUGGCGCCGA 6239
                                                                                                                                                                                                                                                                                                                                 4 LysTrpProTrpTrpProTrpArgArg 12
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MOLECULE TYPE: Genomic RNA

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-466-422-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GARGER, STEPHEN
HOLTZ, R. BARRY
MCCULLOCH, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 6446 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09466422; Patent No. 6303779
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TURPEN, THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 17.2
73.00
100.00%
100.00%
80.22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004
COMPUTER READABLE FORM:
                                                                                             Genomic RNA
   SEQUENCE CHARACTERISTICS:
LENGTH: 6446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                       TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: unknown
                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                           , MOLECULE TYPE:
US-09-037-751-5
                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                            Query Match:
                                                                                                                                                                     Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
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Alignment Scores:

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APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Bradley K.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REPERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT APPLICATION NUMBER: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGRAM
SEQ ID NO 5936
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4031
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-444-281-35 (1-13) x US-08-159-784-1 (1-4031)
      ATTORNES DATE:
ATTORNES/AGENT INFORMATION:
NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REPERRACE/DOCKET NUMBER: 00246/170001
TELECOMMUNICATION NUMBER: 00246/170001
TELEFAX: (617) 542-5070
TELEFAX: (617) 542-5070
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1671 AAATCCTGGTCCTGGTGGCCCTGGAGG 1645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [ndels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-313-224A-5936/c
; Sequence 5936, Application US/09313294A
Datent No. 6476212
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 TrpProTrpTrpProTrp 10
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60.00
77.78%
77.78%
65.93%
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
Query Match:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                 | Sequence 9281, Application US/09252991A | Patent No. 6551795 |
| Patent No. 6551795 | Patent No. 6551795 |
| Generoe 9281, Application US/09252991A |
| Generoe 9281, Application US/09252991A |
| Generoe 9281, Application US/09252991A |
| TILLE OF INVENTION: AERGIGAINGSA FOR DIAGNOSTICS AND THERAPEUTICS |
| TILLE OF INVENTION: AERGIGAINGSA FOR DIAGNOSTICS AND THERAPEUTICS |
| FILLE REFERENCE: 107196.136 |
| CURRENT APPLICATION NUMBER: US/09/252,991A |
| CURRENT FILING DATE: 1998-02-18 |
| PRIOR FILING DATE: 1998-02-18 |
| PRIOR FILING DATE: 1998-07-27 |
| NUMBER OF SEQ ID NOS: 33142 |
| SEQ ID NO 9281 |
| TYPE: DNA |
| TYPE: DNA |
| TYPE: DNA |
| ORGANIAN: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-159-784-1/C
US-08-159-784-1/C
Sequence 1, Application US/08159784
Fatent No. 5643704
Fatent No. 5643704
Fatent No. 5643704
FAURERAL INVERVATION:
APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
TUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boscon
STREET: 225 Franklin Street
CITY: Boscon
STREET: 225 Franklin Street
CITY: Boscon
STREET: 226 Franklin Street
CITY: Boscon
STREET: 226 Franklin Street
CONUTRY: US.A.
ZIP: Dillo-2804
COMPUTER: Boscon
SOFTWER: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
   Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                         US-09-444-281-35 (1-13) x US-09-252-991A-9298 (1-1362)
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Indels:
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63.00
100.00%
100.00%
69.23%
   63.00
100.00%
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69.23%
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PRIOR APPLICATION DATA:
                      Percent Similarity: 1
Best Local Similarity: 1
Query Match: 6
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-252-991A-9281
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APPLICANT: TEN DIJKE, Peter
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: HELDIN, Carl-Henrik
APPLICANT: MIYAZONO, Kohei
APPLICANT: SAMPATH, Kuber T.
TITLE OF INVENTION: Morphogenic Protein-Specific Cell
TITLE OF INVENTION: Surface Receptors and Uses Therefor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Testa, Hurwitz & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-08-658-268B-1
US-08-658-268B-1
; Sequence 1, Application US/08696268B
; Patent No. 5968752
; GENERAL INFORMATION;
; APPLICANT: ICHIOW, HIDENCE
; APPLICANT: NISHITCH, HIDEKI
; APPLICANT: SAMPATH, KUBER T.
; TITLE OF INVENTION: NOVEL SIGNALLING RECEPTOR FOR TITLE OF INVENTION: MORPHOGENIC PROTEINS
; NUMBER OF ENQUENCES: 8
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: MAA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBA PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENT RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATE: US/08/481,337A
PILING DATE: 02-UN-1995
CLASSIFCATION 1943
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, Thomas C.
REGISTRATION NUMBER: CRP-097CP2
TELEPRONE, CAPA 100
TELEPAN: (617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: /product= "Human ALK1"
US-08-481-337A-1
Sequence 1, Application US/08481337A
Patent No. 5863738
GENERAL INFORMATION:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Bost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
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ADDRESSE: Testa, Hurwitz & Thibeault

STREET 125 High St.

CITY: Boston

STATE: NA

COMPUTER: IMA

COMPUTER: IMA

COMPUTER: FLORPY disk

COMPUTER: FLORY TOWN TOWN TOWN

NAME: FLORY TOWN TOWN TOWN

NAME: MEXISTEATION TOWN TOWN

CELEBRANCH (17) 248-7100

COMPUTER: CONA

CONSENTATION: 1.1509

CONE

CONSENTATION: 1.1509

CONE

CONE

CONE

CONE

CONSENTATION: 1.1509

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CONSENTATION: 1.1509

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CONSENTATION: 1.1509

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CONSENTATION: 1.1509

CONE

CON
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Appl

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Sequence 1444, Ap Sequence 7766, Ap Sequence 3716, Ap Sequence 3517, A Sequence 12845, A Sequence 12845, A Sequence 17644, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1557, Ap
Sequence 1245, Ap
Sequence 157, App
Sequence 1, Appli
Sequence 40678, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3798, Ap
Sequence 3798, Ap
Sequence 1131, Ap
Sequence 92875, A
Sequence 132877,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44536, A
Sequence 94574, A
Sequence 94574, A
                                                                                                                                                                                                       Sequence 15, Appl
Sequence 17, Appl
Sequence 19, Appl
Sequence 53929, A
Sequence 321717,
Sequence 53929, A
Sequence 53929, A
                                                                                                                                                                   Sequence 65, Appl
Sequence 25, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 19, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 659, App
Sequence 17642, A
Sequence 321, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4600, Ap
                                                                                    Sequence 30, Appl
Sequence 6, Appli
Sequence 60, Appl
                                                                                                                                     Seguence 5, Appli
 Sequence 32,
Sequence 31,
Sequence 28,
                                                                                                                                                     Sequence 64,
                                                    Sequence 62,
Sequence 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Charma, Maria Marta
APPLICANT: Chen, Yuchen
APPLICANT: Chen, Yuchen
APPLICANT: Cory, Robert
APPLICANT: Cory, Robert
APPLICANT: Cabralda, Jennifer
APPLICANT: Saleman, Dinar
APPLICANT: Saleman, Dinar
APPLICANT: Saleman, Dinar
APPLICANT: Saleman, Dinar
APPLICANT: Metlitskaia, Luba
APPLICANT: Metlitskaia, Luba
APPLICANT: Metlitskaia, Luba
APPLICANT: ANI-INFECTIVE PEPTIDES
FILER REFERENCE: 660081.421
CURRENT APPLICATION NUMBER: US/10/395,896
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
16 US-10-395-896-31

16 US-10-395-896-31

16 US-10-395-896-62

16 US-10-395-896-62

16 US-10-395-896-62

16 US-10-395-896-62

17 US-10-395-896-63

18 US-10-395-896-64

19 US-09-905-52-6

10 US-09-962-52-7

15 US-10-252-773-15

15 US-10-252-773-15

15 US-10-252-773-15

17 US-10-252-773-17

18 US-10-027-632-53929

19 US-09-815-242-7766

9 US-09-815-242-7766

9 US-09-815-242-7766

9 US-09-815-242-7766

9 US-09-815-242-7766

10 US-10-027-632-53929

11 US-10-027-632-53929

12 US-09-815-242-7766

13 US-10-027-632-9577

14 US-10-027-632-9577

15 US-10-027-632-9577

16 US-10-156-761-4600

17 US-10-292-788-1245

18 US-10-156-761-467

19 US-09-997-722-157

19 US-10-292-788-1245

10 US-10-202-788-1245

11 US-10-202-788-1245

12 US-10-027-632-44536

13 US-10-027-632-44536

14 US-10-26-233-4659

15 US-10-282-788-1245

16 US-10-282-94574

17 US-09-932-766-738-859

18 US-10-027-632-94574

19 US-09-820-790-1
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US-10-424-599-92875
US-10-027-632-132877
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     34570
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70.3
70.3
70.3
69.2
69.2
69.2
69.2
67.6
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US-10-395-896-32
                                                                                                                                                                                                                                                                                                                                                                                              , Search time 281.32 Seconds
  (without alignments)
  209.334 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications NA:*

1: /cgn2_6/ptcdata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptcdata/2/pubpna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptcdata/2/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptcdata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptcdata/2/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptcdata/2/pubpna/USO7_NEW_PUB.seq:*
7: /cgn2_6/ptcdata/2/pubpna/USO7_NEW_PUB.seq:*
8: /cgn2_6/ptcdata/2/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptcdata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptcdata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptcdata/2/pubpna/USO8_PUBCOMB.seq:*
12: /cgn2_6/ptcdata/2/pubpna/USO8_PUBCOMB.seq:*
13: /cgn2_6/ptcdata/2/pubpna/USO9_NEW_PUB.seq:*
14: /cgn2_6/ptcdata/2/pubpna/USO0_NEW_PUB.seq:*
15: /cgn2_6/ptcdata/2/pubpna/USIO8_NEW_PUB.seq:*
16: /cgn2_6/ptcdata/2/pubpna/USIO8_PUBCOMB.seq:*
16: /cgn2_6/ptcdata/2/pubpna/USIO8_PUBCOMB.seq:*
16: /cgn2_6/ptcdata/2/pubpna/USIO8_PUBCOMB.seq:*
16: /cgn2_6/ptcdata/2/pubpna/USIO8_PUBCOMB.seq:*
17: /cgn2_6/ptcdata/2/pubpna/USIO8_PUBCOMB.seq:*
18: /cgn2_6/ptcdata/2/pubpna/USIO8_PUBCOMB.seq:*
19: /cgn2_6/ptcdata/2/pubpna/USIO8_PUBCOMB.seq:*
19: /cgn2_6/ptcdata/2/pubpna/USIO8_PUBCOMB.seq:*
19: /cgn2_6/ptcdata/2/pubpna/USIO8_PUBCOMB.seq:*
19: /cgn2_6/ptcdata/2/pubpna/USIO8_PUBCOMB.seq:*
19: /cgn2_6/ptcdata/2/pubpna/USIO8_PUBCOMB.seq:*
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                           OM protein - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                  2941586 seqs, 2264995651 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                               Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                           May 11, 2004, 14:35:33
                                                                                                                                                                                                               1 ILKKWPWWPWRRK 13
                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                              US-09-444-281-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Command line parameters:
                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                               Run on:
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TYPE: DNA ORGANISM: Artificial Sequence

Description

SUMMARIES

Query Score Match Length DB

Result No.

SEQ ID NO 32 LENGIH: 72

N

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139
9.
3
                                                                                                                                                                                                                                                APPLICANT: Guarda, Maria Marta
APPLICANT: Guarda, Macha
APPLICANT: Chen, Yuchen
APPLICANT: Cory, Robert
APPLICANT: Brinkman, Jacqui
APPLICANT: Rabralda, Jennifer
APPLICANT: Suleman, Dinar, TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
TITLE OF INVENTION: ANTI-INFECTIVE PEPTIDES
                                                                                                                                               72
9
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                            Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-444-281-35 (1-13) x US-10-395-896-31 (1-139)
                                                                                                                           US-09-444-281-35 (1-13) x US-10-395-896-32 (1-72)
                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: Exemplary "template" US-10-395-896-31
), OTHER INFORMATION: Exemplary "template" US-10-395-896-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28, Application US/10395896; Publication No. US20030219854A1
                                                                                                                                                                                                                Sequence 31, Application US/10395896 Publication No. US20030219854A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.11
76.00
92.31%
69.23%
83.52%
                                            0.0592
76.00
92.31%
69.23%
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Best Local Similarity: (Query Match:
                                                                    Percent Similarity:
Best Local Similarity:
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                                   Alignment Scores:
Pred. No.:
                                                                                                                                                                                                         US-10-395-896-31
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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DB:
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                                                           Score:
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) OTHER INFORMATION: Nucleic acid template encoding anti-infective (STHER INFORMATION: peptide 11B7 and anionic spacer peptide 511 or 512 US-10-395-896-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 62, Application US/10395896
; Sequence 62, Application US/10395896
; Publication No. US20030219854A1
; GENERAL INFORMATION:
; APPLICANT: Charra, Maria Marta
APPLICANT: Chen, Yuchen
; APPLICANT: Cory, Robert
; APPLICANT: Caralda, Jacqui
APPLICANT: Cabralda, Jacqui
APPLICANT: Cabralda, Luba
APPLICANT: Metlitskaia, Luba
APPLICANT: Metlitskaia, Luba
; APPLICANT: Metlitskaia, Luba
APPLICANT: Metlitskaia, Luba
; TITLE OF INVENTION: MITHON PROPERTIDES
; TITLE OF INVENTION: MATH-INPECTIVE PEPTIDES
; TITLE OF INVENTION: MATH-INPECTIVE PEPTIDES
; TITLE OF INVENTION: ANTI-INPECTIVE PEPTIDES
; CURRENT APPLICATION NUMBER: US/10/395,896
; CURRENT PILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 70
; SEQ ID NO 62
; SEQ ID NO 62
; LENGTH: 121
                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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FILE REFERENCE: 660081.421
CURRENT APPLICATION NUMBER: US/10/395,896
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARER: FASESEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 121
                                                                                                                                                                                                     CTHER INFORMATION: Exemplary "template" US-10-395-896-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 29, Application US/10395896
; Publication No. US20030219854A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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75.00
100.00%
90.00%
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75.00
100.00%
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82.42%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-10-395-896-29
                                                                                                                                                                                                                                                                  Alignment Scores:
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APPLICANT: Cory, Robert
APPLICANT: Cory, Robert
APPLICANT: Brinkman, Jacqui
APPLICANT: Barinkman, Jacqui
APPLICANT: Cabraida, Jennifer
APPLICANT: Mellitskaia, Luba
APPLICANT: Suleman, Dinar
TITLE OF INVENTION: METHODE FOR PRODUCING MODIFIED
TITLE OF INVENTION: ANTI-INFECTIVE PEPTIDES
FILE REFERENCE: 660081.421
CURRENT APPLICATION NUMBER: US/10/395,896
CURRENT APPLICATION NUMBER: 203-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SERGITA 123
TENGTH 1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFBULIO-395-896-30
Sequence 30, Application US/10395896
Sequence 30, Application US/10395896
PUBLICATION OF USZO030219854A1
GENERAL INFORMATION:
APPLICANT: Guarna, Maria Marta
APPLICANT: Cory, Robert
APPLICANT: Cory, Robert
APPLICANT: Brinkman, Jacqui
APPLICANT: Brinkman, Jacqui
APPLICANT: Brinkman, Jacqui
APPLICANT: Suleman, Dinar
TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
TITLE OF INVENTION: ANTI-INFECTIVE PEPTIDES
TITLE OF INVENTION: ANTI-INFECTIVE PEPTIDES
TITLE REFERENCE: 660081.421
STILE REFERENCE: 660081.421
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FRAISEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LysTrpProTrpTrpProTrpArgArgLys 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 CGTTGGCCGTGGTGGCCGTGGCGTAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Exemplary "template" US-10-395-896-30
                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Exemplary "template"
APPLICANT: Guarna, Maria Marta
APPLICANT: Chen, Yuchen
APPLICANT: Cory, Robert
APPLICANT: Brinkman, Jacqui
APPLICANT: Cabralda, Jennifer
                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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75.00
100.00%
90.00%
82.42%
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75.00
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90.00%
82.42%
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Query Match:
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Best Local Similarity:
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Pred. No.:
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APPLICANT: Kairos Scientific, Inc.
APPLICANT: Sylina, Edward J.
APPLICANT: Coleman, William J.
APPLICANT: Bylina, Edward J.
APPLICANT: Coleman, William J.
APPLICANT: Coleman, William J.
APPLICANT: Youvan, Douglas C.
TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR GENERATING
TITLE OF INVENTION: AND SCREENING COMPOUNDS THAT AFFECT CELL VIABILITY
FILE REPRENCE: 22346-7001
CURRENT APPLICATION NUMBER: US/09/909,652
CURRENT FILING DATE: 2001-10-15
PRIOR FILING DATE: 2000-07-19
NUMBER OF SEQ ID NOS: 7
SOFFWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Nucleic acid encoding ubiquitin indolicidin fusion
; OTHER INFORMATION: protein fragment
US-09-909-652-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-LUCYOF GENERAL INCOMMENTION US/10076816

FUBLICARTH NATE OU US20030056244A1

GENERAL INFORMATION:

APPLICANT: Hang, Ning

APPLICANT: Hang, Ning

APPLICANT: Hagle, Frank E.

FILE DE INVENTION: Feed Additive Compositions and Methods

FILE REFERENCE: 50665-8021.0360

CURRENT APPLICATION NUMBER: US/10/076,816

CURRENT ILING DATE: 2002-02-14

FRIOR APPLICATION NUMBER: US 60/269,188

PRIOR FILING DATE: 2001-02-14

PRIOR FILING DATE: 2001-02-05

PRIOR FILING DATE: 2001-02-05

PRIOR FILING DATE: 2001-05-02

PRIOR FILING DATE: 2001-05-05

PRIOR FILING DATE: 2001-05-05

PRIOR APPLICATION NUMBER: US 60/266,929

PRIOR FILING DATE: 2001-05-05

PRIOR FILING DATE: 2001-05-05

SPRIOR PRIOR FILING DATE: 2001-05-05

SPRIOR FILING DATE: 2001-05-05

SPRIOR PRIOR PRIO
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Matches:
Conservative:
Mismatches:
Indels:
US-09-444-281-35 (1-13) x US-09-909-652-6 (1-68)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 LysTrpProTrpTrpProTrpArgArg 12
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                                                                                                                                                                                                     US-09-909-652-6;
; Sequence 6, Application US/09909652;
Patent No. US2002002537A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.133
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; ORGANISM: Bos taurus
US-10-076-816-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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LENGTH: 68
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US-09-444-281-35 (1-13) x US-09-962-527-5 (1-6446)

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4 LysTrpProTrpTrpProTrpArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.513
70.00
100.00%
88.89%
76.92%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
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                                                                             RESULT 10
US-10-395-896-64
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LENGTH: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                    APPLICANT: SALASLA, CALLEY, NICHAEL
HOLTZ, R. BARRY
MCCHLLOCH, MICHAEL
TURPEN, THOMAS
TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
PURIFYING VIRUSES SOLUBLE PROTEINS AND
FROM PLANT SOURCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
CORPATING SYSTEM: DOS
SOSTWARE: PASISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,527
FILING DATE: 24-5ep_2001
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/037,751
FILING DATE: 10-march-1998
ATTORNEY/AGENT INFORMATION:
NAME: HAILUIN, Albert P
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 00801.0140.999
TELEPPAN: 650-463-8400
TELEPPAN: 650-463-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.
CITY: Washington
                                                                                                                                    US-09-444-281-35 (1-13) x US-10-076-816-60 (1-550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: UNLEGATE

MOLECULE TYPE: Genomic RNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-962-527-5
                                                                                                                                                                                                         415 AAATGGCCATGGTGGCCTTGGCGCAGA 441
                                                                                                   Gaps:
                                                                                                                                                                    4 LysTrpProTrpTrpProTrpArgArg 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 6446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                          Sequence 5, Application US/09962527; Publication No. US20030049813A1
GENERAL INFORMATION: APPLICANT: GARGER, STEPHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.69
73.00
100.00%
100.00%
80.22%
            0.953
73.00
100.00%
100.00%
80.22%
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                       Percent Similarity:
Best Local Similarity:
Query Match:
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Alignment Scores:
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TYPE: DNA ORGANISM: Artificial Sequence ORGANISM: Artificial Sequence PERTURE: OTHER INFORMATION: Nucleic acid template encoding precursor peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Nucleic acid template encoding precursor peptide OTHER INFORMATION: 11825 and anionic spacer peptide 521.
                                                                                         GENERAL INFORMATION:
Sequence 64, Application US/10395896
Publication No. US2030219854A1
GENERAL INFORMATION:
APPLICANT: Charan, Maria Marta
APPLICANT: Chen, Yuchen
APPLICANT: Cory, Robert
APPLICANT: Cory, Robert
APPLICANT: Cabralda, Jacqui
APPLICANT: Cabralda, Juda
APPLICANT: Ableman, Jacqui
APPLICANT: Ableman, Juda
APPLICANT: Ableman, Dinar
APPLICANT: Ableman, Dinar
TILE OF INVENTION: METHODS FOR PRODUCING MODIFIED
TILE OF INVENTION: ANTI-INFECTIVE PEPTIDES
TILE REFRENCE: 660081.421
CURRENT APPLICATION NUMBER: US/10/395,896
CURRENT APPLICATION NUMBER: US/10/395,896
CURRENT APPLICATION NUMBER: US/10/395,896
SEQ ID NO 64
INVENTION O 64
INVENTION O 64
INVENTION O 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 65, Application US/10395896

Sequence 65, Application US/10395896

Publication No. US20030219854A1

GENERAL INFORMATION:
APPLICANT: Gharna, Maria Marta
APPLICANT: Chen, Yuchen
APPLICANT: Cory, Robert
APPLICANT: Cabralda, Jennifer
APPLICANT: Cabralda, Jennifer
APPLICANT: Saleman, Jonar
APPLICANT: Saleman, Dinar
TITLE OF INVENTION: METHOUS FOR PRODUCING MODIFIED
TITLE OF INVENTION: METHOUS FOR PRODUCING MODIFIED
TITLE OF INVENTION: MATHONS FOR PRODUCING MODIFIED
TITLE REFERENCE: 660081.421
CURRENT APPLICATION NUMBER: US/10/395,896
CURRENT APPLICATION NUMBER: US/10/395,896
SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-444-281-35 (1-13) x US-10-395-896-64 (1-114)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
6213 Adudeccivideoredeccavececea 6239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
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RESULT 15
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Sequence 25, Application WS/10252773

Publication No. US20030131383A1

GENERAL INFORMATION:
APPLICANT: EVERETY, UICHOLAS P.
APPLICANT: LAY QUNIGSHUN
APPLICANT: LAY QUNIGSHUN
INTILE OF INVENTION: PERPLICES WITH ENHANCED STABILITY TO PROTEASE
TITLE OF INVENTION: PERPLICES WITH ENHANCED STABILITY TO PROTEASE
TITLE OF INVENTION: DEGRADATION
FILE REPREBRUCE: INTERLINE 30-003
CURRENT APPLICATION NUMBER: 30-003
CURRENT PILING DATE: 1998-10-30
FRIOR FILING DATE: 1998-11-02
FRIOR FILING DATE: 1998-11-02
SEQ ID NO 25
LENGHARE: PARENTIN VOICE: 2.1
SEQ ID NO 25
LENGHARE: 207

LENGHARE: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: DNA PCRIL; OTHER INFORMATION: construct US-10-252-773-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15, Application US/10252773
Publication No. US20030131383A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: EVERETT, NICHOLAS P.
APPLICANT: LIAMERNEE, CHRISTOPHER
APPLICANT: LAWERNEE, CHRISTOPHER
TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
TITLE OF INVENTION: DEGRADATION
FILE REFERENCE: INTERLINK 3.0-003
CURRENT APPLICATION NUMBER: US/10/252,773
OTHER INFORMATION: 11B25 and anionic spacer peptide S21
                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                              29 CGTTGGCCGTGGTGCCGTGGCGTCGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.85
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Query Match:
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Best Local Similarity:
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Pred. No.:
                                                                  Alignment Scores:
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US-10-252-773-15
      ; OTHER INFURING ;
US-10-395-896-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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DB:
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APPLICANT: EVERENTI, NICKLAS F.,
APPLICANT: LAWRENCE, CHRISTOPHER
APPLICANT: LAWRENCE, CHRISTOPHER
APPLICANT: LAWRENCE, CHRISTOPHER
TITLE OF INVENTION: PETTIDES WITH ENHANCED STABILITY TO PROTEASE
TITLE OF INVENTION: DERRADATION
FILE REFERENCE: INTERLINK 3.0.003
CURRENT PAPLICATION NUMBER: US/10/252,773
CURRENT PILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/106,573
PRIOR APPLICATION NUMBER: 60/106,573
PRIOR APPLICATION NUMBER: 60/106,573
PRIOR RILING DATE: 1998-110-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE PATENTING VET. 2.1
SEQ ID NO 17
LENGTH: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Primer US-10-252-773-17
                                                                                                                                                                                                                       ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: Oligonucleotide US-10-252-773-15
                                                                                                                                                                                                                                                                                                                  0003
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 LysLysTrpProTrpTrpProTrpArg 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 AGGAGATGGCCTTGGTGGCCTTGGAAA 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGGAGATGGCCTTGGGAA 27
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/106,373
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17, Application US/10252773
Publication No. US20030131383A1
GENERAL INFORMATION:
APPLICANT: EVERETT, NICHOLAS P.
                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4
64.00
100.00%
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64.00
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-10-252-773-17/c
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No..
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Search completed: May 11, 2004, 17:07:32 Job time : 286.32 sec8

US-09-444-281-35 (1-13) x US-10-252-773-19 (1-54)

3 LyslysTrpProTrpTrpProTrpArg 11 ::::::||||||||||||::: 54 AGGAGATGGCCTTGGTGGCCTTGGAAA 28

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

 Run on:
 May 11, 2004, 14:00:48 ; Search time 1721.2 Seconds (without alignments)

 Title:
 US-09-444-281-35

 Perfect score:
 91

 Sequence:
 1 ILKKWPWWPRRK 13

 Scoring table:
 BLOSUM62

Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Command line parameters:

Command line parameters:
-WODE_terame+_parameters:
-WODE_terame+_parameters:
-WODE_terame+_parameters.
-WODE_terame+_parameters.
-WODE_terame+_parameters.
-De_cycpt__1/USPTO_spool/US0944281/runat__07052004_171138_2579/app_query.fasta_1.398
-De_cycpt__1/De_pool/US0944281_rest.-MATRIX=no.1_fCOPCI=0_-LGOPEXT=0
-DOCALIGN=200 -TRR_SCORE=pct_-TRR_NAX=100 -TRR_NIN=0_-ALIGN=15_-WODE_LCCAL
-UNITS=bits -STRAT=1_-SKDE=pct_-TRR_NAX=100_-TRR_NIN=0_-ALIGN=15_-WODE_LCCAL
-UNITS=bits -STRAT=1_-SKORE=pct_-TRR_NAX=0_-MAXLEN=200000000
-USER_SCOPE_scorE=score_NIN_LSN=0_-MAXLEN=2000000000
-USER_SCOPE_SCORE_S

ESI: *

Database :

1: em_estba:*
2: em_esthum:*
3: em_esthum:*
4: em_esthum:*
6: em_estoy:*
6: em_estoy:*
7: em_estoy:*
10: gb_esto:*
11: gb_htc:*
12: gb_esto:*
13: gb_esto:*
14: gb_esto:*
15: em_estfum:*
16: em_estfum:*
17: em_gss_lm:*
18: em_estfum:*
18: em_estfum:*
19: em_gss_lm:*
22: em_gss_lm:*
23: em_gss_lm:*
24: em_gss_lm:*
25: em_gss_lm:*
26: em_gss_lm:*
27: em_gss_lm:*
28: em_gss_lm:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

N		1		5	ç	
	2000	MALCI	Length	9	1	nescription
l		1.3	522	-		479395 RTWW3 2
(7	7.0	76.9	263	12	BI976779	485902
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4	69	5.	σ	28	AZ518927	518927 RPCI-11
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9	68	4.	4	12	BJ476852	76852 BJ47685
7	89	74.7	9	12	BJ474341	74341 BJ47434
œ	68	4.	8	12	BJ471810	10 BJ47181
6	68	4.	Н	12	73	73016 BJ47301
10	69	4.	\vdash	10	9	37369 146
::	689	4.	N	6	AV933841	11 AV93
12	89		4	12	BJ471261	L261 BJ4712
~	89	4	4	σ	^1	2 AU08992
14	68		446	σ	m	4
r.	89	4	4	σ	9	AU19816
19	89	74.7	464	σ	AV935002	302 AV93500
17	89	. 4	-	12	17547	78 BJ47547
20	9 6		. [~	12	BJ475115	5115 BJ4751
0	899	. 4	. [~	12	BJ476710	5710 BJ47671
20	9	74.7	-	σ	AV937233	33 AV937233
21	68	4.	~	12	BJ473880	3880 BJ47
22	68	4.	7	σ	AU089934	34 AU089
23.	68	4.	æ	12	BJ477184	14 BJ47
24	68	4.	0	17	BJ475153	3 BJ47
25	68	4.	501	12	BJ470669	BJ470669 BJ470669
56	68	4.	0	12	BJ475306	6 BJ47
27	68	4.	0	12	BJ471761	1 BJ47
28	68		0	12	BJ473882	32 BJ47
5	89	4	0	12	BJ471258	8 BJ47
0				12	BJ469760	50 BJ46
3	99	4	m	12	BJ472623	3 BJ47
32	89	4	m	12	BJ475836	16 BJ47
33	68		m	6	AV932159	AV93215
34	68	4	m	14	CF326637	37 JMT106
35	68	4.	S	14		JMT106
36	68	4.	വ	14	CF325873	73 JMT1
37	68	4.	~	σ	Ξ	117 AU082117
38	68	4.	9	14	32627	26279 JMT10
39	68	4.	9	14	68116	162 OSJNEFO
40	67	ω.	7	28	55254	52545 pacs1-
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ALIGNMENTS

RESULT 1

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330 bp mRNA linear EST 06-JUN-2000
894003H02.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
BE024584
                                                                                                               USDA, ARS, US Meat Animal Research Center
PO BOX 166, USA
Tel: 402 762 4366
Pax: 402 762 4366
Pax: 402 762 4390
Bmall: anitheemail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
vo.380904.e. Vector identified by cross_match with the -minscore 18
PCR PRIMERS
PCR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P., McDermort, J.P., Silflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2 Unpublished (2000) Contact: Elizabeth H. Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."
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   Senome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="MARC 2BOV"
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Plate: 114 row: F column: 23
Seg primer: ATTTAGGTGACACTATAG.
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/lab_host="DH108"
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Location/Qualifiers
1. .330
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Duke University
Durham, NC 27708-1000, USA
Tel: 919 613 8164
Fax: 919 613 8177
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Contact: Smith TPL
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                                                                                                                                                                                                                                                                                                                                                           EST 23-0CT-2001
                                                                                      An EST database from well-watered loblolly pine (Pinus taeda) roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buxaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Eutheria, Cetartiodactyla, Ruminantia; Pecora, Bovoidea, Bovoidea; Bovoinae; Bovoinae, Bov.

1 (Dases 1 to 263)

Smith, T.P. L., Grosse, W. M., Freking, B. A., Roberts, A. J., Stone, R. T., Casas, F., Mary, J. B., Mite, J., Cho, J., Pahrenkrug, S. C., Casas, F., Harry, J. E., Harron, M. P., Laegreid, W. W., Rohrer, G. M., Chitko-McKown, C. G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J. W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
         Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Dean, J.,
Gebremedhin, M., Dervinis, C., Martin, T., White, T., Davis, J. and
                                                                                                                                                                                                         Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI976779 263 bp mRNA linear 485902 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
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Matches:
Conservative:
Mismatches:
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                                                                                                                     Unpublished (2003)
Other ESTS: RTWW3 23 A01.bl A022
Contact: Cordonnier-Fratt MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pinus taeda"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-444-281-35 (1-13) x CF479395 (1-522)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI976779.1 GI:16351184
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100.00%
72.73%
81.32%
                                                                                                                                                                                                                                                                                                            Tel: 706 542 1860
Fax: 706 583 0210
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Best Local Similarity:
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Pred. No.:
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BI976779
                  AUTHORS
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AG185290 757 bp DNA linear GSS 09-JAN-2002
Pan troglodytes DNA, clone: RP43-059F08.TJ, genomic survey
sequence.
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                           /cell_type="Lymphocytes"
/colne_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Unpublished
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Mismatches:
Indels:
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                            Length:
Matches:
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/db_xref="GDB:7525385"
/db_xref="taxon:9606"
/clone="RPCI-11-67B18"
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-444-281-35 (1-13) x AZ518927 (1-390)
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R.Site 1 : ECORI
R.Site 2 : ECORI.
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                                                                                            /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Bex="male"
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                                                                                                                              Anote—"Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
Xho1; This library, constructed by John Davies and Jeffrey
McDermock, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA,
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites,
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

B. 1 (bases 1 to 390)

S. Saoo,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

BAC end sequences of library RPCI-11

L. Unpublished (1997)

Other GSSs: RPCIII-67818.TJ

Contact: Sharing Zhao

Department of Enkaryotic Genomics
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390 bp DNA linear GSS 16-OCT-2000 RPCI-11-67B18.TV RPCI-11 Homo sapiens genomic clone RPCI-11-67B18, agenomic survey sequence.
                                                                                            'clone lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: szhao@tigy.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
library availability, please contact Pieter de Jong
(pieter@delong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@tesgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
This BAC end was generated during the R&D process and may have
higher chance of clone tracking errors.
    organism="Chlamydomonas reinhardtii"
                                       /strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
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Homo sapiens
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RESULT 4 AZ518927/c LOCUS DEFINITION

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SOURCE ORGANISM

TITLE JOURNAL COMMENT

AUTHORS

REFERENCE

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FEATURES

Alignment Scores:

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Pred. No.:

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381 bp mRNA linear EST 23-MAY-2002 BJ471810 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baal21m20 5', mRNA sequence.
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermarophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooideae; Iriticeae; Hordeum.
             Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 369)
Sato,K., Saisho,D. and Takeda,K.
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="top three leaves"
/dev stage="adult, heading stage"
/dor_elih="kr. Sato umpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"
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Sato,K., Saisho,D. and Takeda,K.
Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                              /organism="Hordeum vulgare subsp. vulgare"
/mol type="mRNA"
/cultivar=Haruna Nijo"
/sub_specie="vulgare"
/db xref="taxon:112509"
/clone="baal13e18"
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National Institute of Genetics
Inil Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 91-55-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                           Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Ill Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Location/Qualifiers
1. .381
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Location/Qualifiers
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BJ471810/c
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                                                                                                                                                                                                                                                             linear EST 23-MAY-2002
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae, Triticeae, Hordeum.

1 (bases 1 to 349)
Sato, X., Saisho, D. and Takeda, K.
Unpublished (2002)
                                                                                                                                                                                                                                                       BJ476852 K. Sato unpublished cDNA library, cv. Haruma Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA EJONE BJ476852 K. Bathana Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA BJ476852
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|cultivar="Haruna Nijo"
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|tissue type="top three leaves"
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|clone lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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BJ474341
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Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Pooideae; Triticeae; Hordeum.
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Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
Contact: Tadasus Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishims, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
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/dev gtage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA_library
Nijo adult, heading stage top three leaves"
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|mol_type="mRNA"
|cultivar="Haruna Nijo"
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(db xref="taxon:112509"
/clone="baal40h02"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               183 TGGCCGTGGTGGCCGTGGCGGCGA 160
                                                                                                                                                                                                                                                                                                            US-09-444-281-35 (1-13) x BJ471810 (1-381)
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BJ473016.1 GI:21151519
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US-09-444-281-35 (1-13) x BJ473016 (1-411)

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Bos taurus (cow)

Mos taurus

Bus taurus

Bus taurus

Bus taurus

Bus taurus

Bus taurus

Bus taurus

Businas;

Butheria;

Cetartiodactyla;

Ruminantia;

Bovidae;

Bovidae;

Bovidae;

Bovidae;

Bovidae;

Bovidae;

Bovidae;

Casas, E., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,

Bennett, G.L., Heaton, M.P., Laegried, W.W., Rohrer, G.A.,

Chitko-McKown, C.G., Perrea, G., Molt, I., Karamycheva, S., Liang, F.,

Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

L. Genome Res. 11 (4), 626-630 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. vector identified by cross_match with the -minscore 18
           EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue From day 20 and day 40
embryos."
415 pp mRNA linear
146629 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
BE227369
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USDA, ARS, US Meat Animal Research Center
PD Box 166, Clay Center, NE 68933-0166, USA
PEL 1402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
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/organism="Bos taurus"
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/tissue_type="pooled"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 47 row: J column: 10
Seg primer: ATTTAGGTGACTATAG.
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PCR PRimers
                                                                                        BE237369.1 GI:9022087
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Gaps:
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                                                                 /mol_type="mRNA"
/cultivar="Haruna Nijo"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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BJ471261 GI:21149764
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (basea 1 to 440)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
                                                                                Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (Dases I to 420)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2022)
heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA clone baal9005 5', mRNA sequence.
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/dev_stage="adult, heading stage"
/clone_lib="k. Sato unpublished cDNA library, cv. Haruna
Nijo adult, heading stage top three leaves"
                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare subsp. vulgare"
/mol type="mRNA"
/cultivar="Haruna Nijo"
                                                                                                                                                                                                                                              Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@qenes.nig.ac.jp.
Location/Qualifiers
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National Institute of Genetics
Ill Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Matches:
Conservative:
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Indels:
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/db_xref="taxon:112509"
/clone="baa19005"
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                                                      AV933841.1 GI:18229638
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100.00%
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Best Local Similarity:
                                       AV933841
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AU089922 Hordeum vulgare subsp. vulgare Upper three leaves at haruna libilizi, mRNA sequence.

AU089922 Hordeum vulgare subsp. vulgare cDNA clone haruna libilizi, mRNA sequence.

AU089922 AU089922.1 GI:7613350
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
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| bb_xref="texon:112509"
| clone="baal17107"
| tissue_type="top three leaves"
| dev stage="adult, heading stage"
| clone lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sub_species="vulgare" | /db_xref="taxon:112509" | /clone="haruna lib1_121" | /rissue_type="Upper three leaves at heading stage" | /clone lib="Hardeum vulgare subsp. vulgare Upper three leaves at heading stage" |
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|mol_type="mRNA"
|cultivar="Haruna Nijo"
/organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kazuhiro Sato
Research Institute for Bioresources
Cokayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: Kazastoerib. Okayama "u.ac.jp,
URi:http://www.rib.okayama-u.ac.jp/barley/.
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0 0
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Matches:
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Mismatches:
Indels:
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Hordeum vulgare subsp. vulgare cDNA clone
Unpublished (2000)
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Matches:
Conservative:
Mismatches:
Indels:
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Search completed: May 11, 2004, 16:56:32 Job time : 1725.2 secs
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Best Local Similarity:
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                                                                                                                                                                       AUI98144 Rice green shoot Oryza sativa (japonica cultivar-group) cDNA clone SI5951, mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (Dases I to 448)
Sasaki, T. and Yamanoto, K.
Rice cDNA from green shoot (2001)
                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (Dases 1 to 446)
Sasaki, T. and Yamamoto, K.
Rice cDNA from green shoot (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contract: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasski@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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Matches:
Conservative:
Mismatches:
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/clone="615951"
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/note="Green shoot (8 days old)
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                      US-09-444-281-35 (1-13) x AU089922 (1-446)
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AU198144/c
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Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
1918-18-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'.
                                                                                                                                         4448
7 7 1
1 0 0
                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                               314 CGCCGCTGGCCTTGGTGGCCCTGGACGCGGCGG 282
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                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                      US-09-444-281-35 (1-13) x AU198162 (1-448)
                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                            612
68.00
90.91%
63.64%
Unpublished (2001)
                                                                                                                                 1. .448
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BC028879
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BD103482
AF166097
AC132933
AC1329212
AC102491
AX354516
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AX098418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Command line parameters:
-MODEL=frame+_pDn.model -DEW=xlh
-Q=/cgn2_1/USPTO_spool/USO344281/runat_07052004_171138_2568/app_query.fasta_1.398
-Q=/cgn2_1/USPTO_spool/USO344281/runat_07052004_171138_2568/app_query.fasta_1.398
-Q=/cgn2_1/USPTO_spool/USO3444281/runat_07052004_171138_2568_0._LOOPEXT=0
-UNITS=bits -START=1 -NND=1 -NATRIX=biosum62 -TRANS=bumman40.cdi -LIST=45
-DOOLIGN=200 -THR_SCORB=pt_-THR_MAX=100 -TRR_MN=0 -ALIGN=15 -MODE=LOCAL
-UNFRT=pto -NORM=ext -HEAPSIZE=500 -MINILEN=0 -MAXIEN=2000000000
-USER=USO3444281_@CGN 1 1 3608_@runat_07052004_171138_2568_NOPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBECCK=100 -LONGIGG
-DBV_TINEOUT=120 -NARN TIMEOUT=30 -TRREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELCP=6 -DELEXT=7
                                                                                                                                                         May 11, 2004, 13:53:18; Search time 2221.92 Seconds (without alignments) 234.084 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6940544
                        GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                - nucleic search, using frame plus p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                 Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                              Run on:
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X67340 Bos faurus AR17324 Sequence AX098418 Sequence AL672300 Mouse DNA AC113900 Rattus no AC055460 Rattus no U08210 Mus musculu

BD247523 Method fo BD247529 Method fo BD247520 Method fo BD247517 Method fo AX357080 Sequence

Description

AX357080 Sequence BD128612 Method fo AR404925 Sequence AR226388 Sequence AR282754 Sequence

AP004382 Oryza sat AC091250 Mus muscu AJ300832 Delftia a Continuation (8 of BD273664 Peptides

AF210429 Mus muscu BC028879 Mus muscu

BC051649 Mus muscu AF289665 Mus muscu

AF166097 Mus muscu AC132933 Mus muscu AC120860 Mus muscu AC139212 Mus muscu AC102491 Mus muscu

Trypanoso Trypanoso

AY354516 T AC104488 T

Peptides Peptides

Peptides Corynebac

APO03141 Oryza sat BC029697 Mus muscu

Z22923 M.musculus

AC005724 Arabidops AP003141 Oryza sat

X17342 Arabidopsis L09262 Arabidopsis

AX653694 Sequence

Mus muscu

BD095993 Immunoass BD103482 Immunoass

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M BD247520.1 GI:33057290
S 9702530114-A/14.
S 9702530114-A/14.
S synthetic construct
ESM synthetic construct
artificial sequences.
E 1 (bases I to 151)
S Burian, J. and Bartfeld, D.
Method for effectively producing antibacterial cationic peptides in host cells
AL Patent: JP 2002530114-A 14 17-SEP-2002;
MICROLOGIX BIOTECH INC
OS Artificial Sequence
PN JP 2005530114-A/14
PD 17-SEP-2002
PN JP 2005530114-A/14
PN JP 200530114-A/14
PN JP 2005530114-A/14
PN JP 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BD247520 151 bp DNA linear PAT 17-JUL-2003 Method for effectively producing antibacterial cationic peptides in host cells.
C12N15/09,C07K1/12,C07K1/18,C12N1/15,C12N1/19,C12N1/21,C12P21/
02//
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Synthesized oligonucleotide used as a template for PCR
Location/Qualifiers
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                                                           (Ci2p21/02,Cl2R1:19),Cl2N15/00
Synthesized oligonucleotide used as a template
Location/Qualifiers
                                                                                                                    ce 1. .114
/organism='Artificial Sequence'
Location/Qualifiers
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Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
Indels:
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                 1. .114
/organiss="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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DEFINITION
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AUTHORS
TITLE
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BD247520
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Synthetic construct
artificial sequences.

1 (bases 1 to 114)

Burian, J. and Bartfeld, D.
Method for effectively producing antibacterial cationic peptides in host cells
MICROLOGIX BIOTECH INC

OS Artificial Sequence
FN JP 2002530114-A/23

PD 17-SEP-2002,
PP 19-NOV-1999 JP 2000584088

PR 20-NOV-1999 US 60/109218

PI JAN BURIAN, DANIEL BARTFELD
                                                                                                                                                                                                                                                Burian, J. and Bartfeld, D. Method for effectively producing antibacterial cationic peptides in
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                                            BD247523 17-JUL-2003 Method for effectively producing antibacterial cationic peptides in
                                                                                                                                                                                                                                                                                                                                             Artificial Sequence
17-20230114-A/17
17-SEP-2002
19-NOV-1999 JP 2000584088
20 NOV-1998 US 60/109218
JAN BURIAN, DANELE BARTPELD
CIRNIS/09,CO7KI/12,CO7KI/18,C12N1/19,C12N1/21,C12P21/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
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Synthesized oligonucleotide us as a template for PCR FH
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..108
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/db_xref="teaxon:22630"
                                                                                                                                                                                                                                                                                        host cells
Patent: JP 2002530114-A 17 17-SEP-2002;
MICROLOGIX BIOTECH INC
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                                                                                                   BD247523
BD247523 GI:33057293
JP 200530114-A/17.
Synthetic construct
synthetic construct
artificial sequences.
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JP 2002530114-A/23.
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Best Local Similarity: 1
Query Match: 1
DB: 6
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BD247529
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PAT 18-SEP-2002
                1..68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indolicidin gene
JP 200250246-A/15
22-JAN-2002
28-MAY-1999 JP 1999500514
28-MAY-1997 KR 1997/21312,09-APR-1998 KR 1998/13372 PI
CHANG KIM,JAE HYUN LEE,MIN HYUNG KANG,JEONG HYUN KIM,SEUNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unclassified.

1 (bases 1 to 39)
Kim,S.C., Lee,J.H., Kang,M.H., Kim,J.H., Hong,S.S. and Lee,H.S. Method for mass production of antimicrobial peptide
Patent: JP 20022502246-A 15 22-JAN-2002,
SAMYANG GENEX CORP, KOREA ADVANCED INSTITUTE OF SCIENCE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYUN SOO LEB
C12M15/62
Methof for mass production of antimicrobial peptide FH
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  BD128612 39 bp DNA linear
Method for mass production of antimicrobial peptide.
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Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                               28 TTGAAATGGCCTTGGTGGCCTTGGCGTCGC 57
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Location/Qualifiers
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BD128612.1 GT:23223557
JP 2002502246-A/15.
unidentified
unidentified
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90.00%
86.05%
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88.89%
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Best Local Similarity:
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Pred. No.:
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BD128612
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JP 2002530114-A/11.
Synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 114)
Burian, J. and Bartfeld, D.
Method for effectively producing antibacterial cationic peptides in host cells
Patent: JP 2002530114-A 11 17-SEP-2002;
MICROLOGIX BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bylina, E.J., Coleman, W.J. and Youvan, D.C.
High-throughput methods for generating and screening compounds that
affect cell viability
Patent: WO 0206517-A 6 24-JAN-2002;
Kairos Scientific, Inc. (US)
                                                                                                                  BD247517 11-JUL-2003 Method for effectively producing antibacterial cationic peptides in host cells.
                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1999 JP 2000584088
20-NOV-1998 US 60/109218
JAN BUXIAN, DANTEL BARFELD
CIZNIS/09, COTKI/12, COTKI/18, CIZNI/15, CIZNI/19, CIZNI/21, CIZP21/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT 13-FEB-2002
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Synthesized oligonucleotide used as a template for PCR
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
                               1. .114
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Sequence from Patent W00206517.
AX357080 1 GI:18674262
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      US-09-444-281-36 (1-12) x BD247520 (1-151)
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JP 2002530114-A/11
17-SEP-2002
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Best Local Similarity:
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Pred. No.:
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BD247517
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KEYWORDS
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AX357080
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Key

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13. .447
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  AR282754.1 GI:29719494
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70.00
100.00%
88.89%
81.40%
                                             Unknown.
Unclassified.
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Best Local Similarity:
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                                Unknown.
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                         PAT 18-DEC-2003
                                                                                                                This force ito 69)

Wood, T.K., Jayaraman, A. and Barthman, J.C.
Inhibition of sulfate-reducing-bacteria-mediated degradation using bacteria which secrete antimicrobials
Patent: US 6530197-A 1 07-0CT-2003;
Location/Qualifiers
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                          linear
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Matches:
Conservative:
Mismatches:
Indels:
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Selsted, M.E. and Osapay, K.
Crosslink stabilized indolicidin analogs
Patent: US 6444645-A 11 03-SEP-2002;
Location/Qualifiers
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AR226388
AR226388.1 GI:27264888
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                         AR404925 69 bp
Sequence 1 from patent US 6630197.
AR404925
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Best Local Similarity:
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Best Local Similarity:
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Pred. No.:
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AR282754
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AR226388
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               AR404925
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/db_xref="SHSS-PROT:P33046"
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INELSSEANLYRLILELDPPPRONEDLGTRREVSFTVKETVCFRTIQQPAEGCDFKEKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAM 15-NOV-2001
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S Del Sal,G
Direct Submission
L Sold Sal, Univ. of Trieste, Dip. di
Biochimica, Biofisica e Chimica, delle Macromolecole, Via A.
Valerio, 38, 34127 Trieste, ITALY
Location/Qualifiers
L Sold Submission
Mol Lype="MRNA"

/ Mol Lype="MRNA"
/ Mol Exref="taxon:9913"
/ GeI line="bone marrow cells"
/ Geo-"CATHL4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Del Sal,G., Storici,P., Schneider,C., Romeo,D. and Zanetti,M. cDNA cloning of the neutrophil bactericidal peptide indolicidin Biochem. Biophys. Res. Commun. 187 (1), 467-472 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X67340.1 GI:462
cathelicidin; CATHL4 gene; indolicidin antimicrobial peptide.
Bos taurus (cow)
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function="indolicidin antimicrobial peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                550 bp mRNA linear
Bos taurus mRNA for cathelicidin (CATHL4 gene).
X67340
(bases 1 to 211)
Selsted, M. E.
Indolicidin analogs and methods of using same
Patent: US 6524585-A 38 25-FEB-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 ArgTrpProTrpTrpProTrpArgArg 11
                                                                                                                                                                     /organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 AAArddccarddragcccarddcarcar 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-444-281-36 (1-12) x AR282754 (1-211)
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Patent: WO 0119969-A 5 22-MAR-2001;
Large Scale Biology Corporation (US)
Location/Qualifiers
                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                               sequence.
AL672300
                                                                                                                            Alignment Scores:
                                                                                                                                                                                               Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                          Pred. No.:
                                                                                                                                                                                                                                                                                                                           RESULT 13
AL672300
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
JOURNAL
    JOURNAL
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                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garger,S.J., Holtz,B.R., Mcculloch,M.J. and Turpen,T.H.
A process for isolating and purifying viruses, soluble proteins and
peptides from plant sources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT 03-APR-2001
                                                                                                                                                                                                                                                                                                                                        PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Unclassified.
1 (bases I to 6446)
Garger, 5.J., Holtz,R.Barry., McCulloch,M.J. and Turpen,T.H. Process for isolating and purifying viruses and sugars from plant
 RVKQCVGTVTLDPSNDQFDLNCNELQSVILPWKWPWWPWRRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Matches:
Conservative:
Mismatches:
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Matches:
Conservative:
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                                                                                                                                                                      Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: US 6303779-A 5 16-OCT-2001;
                                                                                                                                                                                                                                                                                                                                        AR173324 6446 bp
Sequence 5 from patent US 6303779.
AR173324 AR173324.1 GI:17912815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AX098418 6446 bp
Sequence 5 from Patent W00119969.
AX098418
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                13. .99
/gene="CATHL4"
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Nicotiana benthamiana
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Best Local Similarity:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
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                                                                                                              Alignment Scores:
Pred. No.:
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                 sig_peptide
                                              mat peptide
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KEYWORDS
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
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AL Submission

AL Submission

Submitted (14-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Direct Submission

Submitted (14-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On un 17, 2002 this sequence version replaced gi:21261899.

During sequence asembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission or responding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phread quality >= 30); an attempt was made to resolve all sequencing problems, such as semily was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORWIPEP; Information on the WORWIPEP from the REDC-23 Mouse PAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm

VECTOR: pBACE3.6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL672300 14-JUN-2002 DNA linear ROD 14-JUN-2002 Mouse DNA sequence from clone RP23-446K8 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukarnalia; Butheriai, Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 149991)
1. 6446
/organism="Nicotiana benthamiana"
/mol_type="unassigned RNA"
/db_xref="taxon:4100"
                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
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    149991
    organism="Mus musculus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP23-446K8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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70.00
100.00%
88.89%
81.40%
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Score:

à

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misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marzny, Dawles, Ito 195/81, Allen, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H., Balabrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H., Balari, V., Blair, J., Blarkenburg, K., Bryth, P., Brown, M., Bersalo, K., Blair, J., Blarkenburg, K., Bryth, P., Brown, M., Bryant, M., Balari, J., Barken, J., Cabaco, I., Casasz, H., Center, A., Chacko, J., Chan, S., Chen, Z., Chu, J., Chacko, J., Chave, D., Chen, G., Chen, S., Chen, S., Chen, S., Chen, S., Chen, S., Chen, S., Chacko, J., Chave, S., Chen, S., Chen, S., Chen, S., Chen, S., Chacko, J., Charas, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Beyart, M., Bogan-Rochas, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, G., Perandez, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Engen, C., Eling, Y., Garcis, M., Gabisi, A., Ganes, S., Dunn, A., Garcis, M., Garcis, M., Gabisi, A., Ganes, J., Garcis, M., Garcis, M., Handel, P., Haaland, W., Hamilton, C., Hamilton, K., Hanilton, S., Haldun, S.L., Hodgerson, A., Henderson, M., Hernandez, K., Hilles, S., Haldun, S.L., Hodgerson, A., Henderson, K., Kovar, C., Kowai, G., Kath, C., L., Lebow, H., Levan, J., Lui, J., Liu, M., Liu, Y., Lindon, H., Martin, K., Marin, K., Peraco, M., Olivoz, J., Hachlin, E., Soett, G., Sharen, K., Sander, K., Shrarebey, R., Schere, K., Sch
                                                                                                                                                                                                                                                                                                                                                                                                                                 195764 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH230-328H11, *** SEQUENCING IN PROGRESS
***, 2 unordered pieces.
ACL13900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC113900.5 GI:25007914
HTG; HTGS-PHASEI; HTGS_BNRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                             12272 ATATGGAGGTGGCCATGGTGGCCCTGGCGC 12301
                                                                                                                                                                                                                                                                                        1 lleLeuArgTrpProTrpTrpProTrpArg 10
                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                 US-09-444-281-36 (1-12) x AL672300 (1-149991)
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                              3.3e+03
                                                                               90.00%
90.00%
81.40%
                                                                                                                Best Local Similarity:
                                                                                     Percent Similarity:
Alignment Scores:
Pred. No.:
                                                                                                                                               Query Match:
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KEYWORDS
SOURCE
ORGANISM
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LOCUS
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Direct Submission

Direct Submission

Direct Submission

Direct Submission

Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

CB 3 (Dasse 1 to 155764)

Rat Genome Sequencing Consortium.

Direct Submission

AL Submitted (15-NOV-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23662809.

The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (Http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold') within each contig-scaffold' within each contig-scaffold' within each contig-scaffold by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence reads.
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* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces as in not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: C120-328H11

------ Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 15810 bases at least Q40

Consensus quality: 15811 bases at least Q30

Consensus quality: 158110 bases at least Q30

Entimated insert size: 158216; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Ye, T., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Center
Center: Baylor College of Medicine
Center: Cade: BCM
Genter code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contear: hgc-help@bcm.tmc.edu
Contear: project Information
Center project name: GTAQ
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/mol_type="genomic DNA"
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/note="wgs_end_extension
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/note="clone_boundary
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Unpublished
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REFERENCE
AUTHORS
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       In the series, Merker, M. Lee., Abramzon, S., Adams, C., Alder, J., Bardarin, D., Bandarin, D., Barder, J., Chen, Y., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Y., Chen, Z., Chen, Z., Chen, Y., Chen, Y., Chen, Z., Chen, Z., Chen, Y., Chen, Z., Chen, Z., Chen, J., Chen, Y., Chen, Z., Chen, Z., Chen, Y., Chen, Z., Chen, Z., Chen, Y., Chen, Z., Chen, Z., Chen, Z., Chen, Y., Chen, Z., Chen, Z., Chen, Y., Din, H., Davis, C., Devreland, C., Cokrell, R., Cox, C., Coyle, M., Cree, A., Dival, B., Davis, C., Devreland, C., Cokrell, R., Cox, C., Coyle, M., Cherer, M., Gerer, M., Davis, C., Davy-Carroll, L., Davis, C., Ding, Y., Din, H., Diva, J., Eagle, C., France, C., Mara, C., Ding, Y., Din, H., Diva, J., Eagle, C., France, C., Falle, J., Eagle, C., France, C., Falle, J., Eagle, C., France, C., France, C., Hamiton, C., Hamiton, C., Hamiton, K., Gerer, M., Hadun, S.L., Henderson, M., Hadun, S., Huly, S., Hune, J., Talebird, D., Jackson, L., Jang, H., Johnson, R., Johnson, J., Lu, X., Ma, J., Lu, Y., Ma, J., Lu, Y., Ma, J., Lu, Y., Ma, J., Lu, Y., Man, J., Lu, Y., Ma, J., Lu, Y., Man, J., Lu, Y., Ma, J., Ma, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACO95460 255121 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-7JB, WORKING DRAFT SEQUENCE.
ACO95460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP. Rattus norvegicus (Norway rat)
                                                                                                                                                                                   Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187911 AGGTGGCCATGGTGGCCATGGAAGCGG 187937
                                                                                                                                                                                                                                                                                                             Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 ArgTrpProTrpTrpProTrpArgArg 11
end_sequence:BZ164864"
109081. .110233
                                                                /note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC095460.6 GI:30467723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 255121)
                                                                                                                                                                                   4.34e+03
70.00
100.00%
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81.40%
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                                                                                                                                                                                                                                                Percent Similarity:
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                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                         Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                                                         Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC095460
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
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Submitted (19-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA on May 9, 2003 this sequence version replaced gi:24941100. The sequence in this sequence version replaced gi:24941100. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Worley, K.C.
Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (Dasses It to 255121)
Stat Genome Sequencing Consortium.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a "working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vallasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., Milte, F., Walliams, G., Williams, G., Williams, G., Williams, R., Whu, J., Yakub, S., Yen, J., Yoon, L., Yoon, Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 243644 bases at least Q40
Consensus quality: 245664 bases at least Q30
Consensus quality: 246956 bases at least Q30
Estimated insert size: 260749; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 255121: contig of 255121 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine
Center code: BCM
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/db_xref="taxon:10116"
/clone="CH230-7J8"
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                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
2 (bases 1 to 255121)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1, 1163
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/note="wgs_contig"

misc_feature 252824. .255121 /note="wgs_contig"

ORIGIN

5.7e+03 70.00 100.00% 88.89% 81.40% Alignment Scores:

Pred. No:
Score:
Fercent Similarity:
Best Local Similarity:
DB:
DB:

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

255121 8 1 0 0

US-09-444-281-36 (1-12) x AC095460 (1-255121)

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Search completed: May 11, 2004, 16:01:51 Job time: 2243.92 secs

Perfect score:

Title:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

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Oligonucleotide; cellulose binding domain; CBD; cationic peptide; MBI-11;
                                                                                                                                                                                                                    Primer RI
Tobacco P
            DNA fragm
DNA fragm
Antimicro
                                                                                                                             Tobacco m
PCRIL DNA
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TMV-based
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Mouse X-t
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Antibacte
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Drosophil
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Drosophil
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Genomic 5
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Ab122542 D
                                                                                                                                                                                                                                                                                                                                                                                          Aas79653
Aas75627 |
Ab115825 |
Aaz46155
Aaz29390
Ab160414
Ab160415
Aaz29364
Ab160445
Ab3240246
                                                                            Aaz49764
Aaz45123
Aad45350
                                                                                                                  Aaz20646
Aaf82334
                                                                                                                                                       Ab158680
Aba96630
                                                                                                                                                                                 Aaa28510
Adc73335
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Adc73337
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Ada70241 1
Aas54129
                                                                                                                                                                                                                                                                                                              Aca51647
Ab121536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide used for synthesis of MBI 2X11B7 poly cassette.
                                                                                                                                           Aaa28519
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                                                  ABL60445
AAZ40246
AAZ40246
AAZ49774
AAZ45123
AAZ45350
AAZ20646
AAR22334
AAR28119
ABL58680
ABL58680
ABAS6819
ABAS6819
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AAA28512
ADC73337
ADC73339
ADA70241
AAS54129
ABL21537
AAS56079
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ADB52723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-CA001107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0109218P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA27296 standard; DNA; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
    indolicidin; bovine; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Burian J, Bartfeld D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-400086/34.
                                                                                                      WO200031279-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-2000.
  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA27296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA27296
    Command line parameters:
-MODEL-Frame+ p2n.model -DEV=xlh
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -NATRIX=blosum62 -TRANS=human40.cdi
-LISP=45 -DOOALIGN=500 -THR SCORE=pct -THR NAX=-100 -THR NIN=0 -ALIGN=15
-USFR=USO344281 @CGN_1_1_S86_@runat_07052004_171138_2561_NCPU=6 -ICPU=3
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-NOGRES=0 -WAIT -SSPENDS-1 - SGAROPES-1 - AGAROPES-1 - AGAROPES-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aaa27296 Oligonucl
Aaa27294 Oligonucl
Aaa27294 Oligonucl
Aav60908 DNA fragm
Aaa27291 Oligonucl
Aay12481 Oligonucl
Aav83788 Antimicro
Aaz29389 PCR prime
                                                                                           May 11, 2004, 12:39:07; Search time 237.12 Seconds (without alignments) 214.990 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                      6747726
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                  nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                             3373863 seqs, 2124099041 residues
                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
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AAA27294
AAV60908
AAA27291
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AAV83788
AAZ29389
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Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext 0
Fgapop 6.0 , Fgapext Delop 6.0 , Delext
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geneseqn2001as:*
geneseqn2001bs:*
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geneseqn2004s:*
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geneseqn1990s:*
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Maximum DB seq length: 200000000
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86
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Match Length DB
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1114
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39
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87.2
86.0
81.4
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Database

86 86 86 75 75 70 70

Result Ñ.

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be used as antimicrobial agents. The present sequence is an oligomorlectide that was used to synthesise a MBI-11B7 fragment. This fragment was used in the expression cassette. MBI-11B7 is a cationic peptide derived from modifications of indolicidin
                                                                                                                                                    Sequence 114 BP; 20 A; 34 C; 32 G; 28 T; 0 U; 0 Other;
         $$$$$$$$
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                                                         A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multidomain fusion protein expression casestre comprising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of positive charge of the cationic peptide sequences in the linker sequences neutralises the positive charge of the cationic peptide so that the charge of the fusion protein is controlled. This cassette allows high yield, stable production of the cationic peptide. Cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligonuclectide that was used to synthesise a MBI-11B7 fragment. This fragment was used in the expression cassette. MBI-11B7 is a cationic peptide derived from modifications of indolicidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide; cellulose binding domain; CBD; cationic peptide; MBI-11;
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stable production of foreign peptide gene products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide used for synthesis of MBI 11B7 first cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 108 BP; 18 A; 33 C; 31 G; 26 T; 0 U; 0 Other;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-444-281-36 (1-12) x AAA27296 (1-108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 40; 73pp; English.
            Example 5; Page 39; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA27298 standard; DNA; 114 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-CA001107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0109218P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0254
86.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 indolicidin; bovine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bartfeld D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-400086/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200031279-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUN-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA27298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA27298
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A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multi-domain fusion protein expression cassette comprising a promoter and annucleic acid molecule expressed as an insoluble protein. The inclusion of anionic peptide expressed as an insoluble protein. The inclusion of anionic peptide sequences in the linker sequences neutralises the posteitive charge of the cationic peptide so that the charge of the fusion of the cationic peptides but the charge of the fusion of the cationic peptide. Cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an obligination chargener was used to synthesise a MBI-11B7 fragment. This fragment was used in the expression casette. MBI-11B7 is a cationic
                                                                                                                                                                                                                                                                                                                                                                    cellulose binding domain; CBD; cationic peptide; MBI-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multi-domain fusion protein expression cassette used for high yield stable production of foreign peptide gene products.
                                                                                                                                                                                                                                                                                                                                         Oligonucleotide used for synthesis of MBI 2X11B7 last cassette.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 151 BP; 22 A; 44 C; 49 G; 36 T; 0 U; 0 Other;
           114
12
0
0
0
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12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide derived from modifications of indolicidin
                                                                                                                                                   12
                          Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                       47 ATTCTGCGTTGGCCGTGGTGGCCGTGGCGTAA 82
                                                                                                                                                     1 IleLeuArgTrpProTrpTrpProTrpArgArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
         Length:
                                                                                        Gaps:
                                                                                                                     (1-114)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                               BP.
                                                                                                                       US-09-444-281-36 (1-12) x AAA27298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-CA001107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0109218P.
                                                                                                                                                                                                                                                AAA27294 standard; DNA; 151
                           86.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.036I
86.00
             0.0269
                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide; cellulc
indolicidin; bovine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burian J, Bartfeld D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-400086/34.
                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200031279-A2.
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                                                                                                                                                                                                                                                                                                             20-SEP-2000
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Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-2000.
Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                               AAA27294;
                                                                         Query Match:
                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                 AAA27294
                               Score:
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12

BP

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A novel method allows the efficient production of cationic peptides in recombinant host cells. The method involves construction of a multidomain fusion protein expression cassette compitising a promoter and a nucleic acid molecule expressed as an insoluble protein. The inclusion of positive charge of the cationic peptide so that the charge of the fusion peried so that the charge of the fusion of the cationic peptide so that the charge of the fusion of the cationic peptides. Cationic peptides such as bovine indolicidin may be used as antimicrobial agents. The present sequence is an oligonucleotide that was used to synthesise a MBI-11 fragment. MBI-11 is a cationic peptide derived from modifications of indolicidin
                                                                                                                                                                                                                                                                                                              Oligonucleotide, cellulose binding domain; CBD; cationic peptide; MBI-11; indolicidin; bovine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multi-domain fusion protein expression cassette used for high yield stable production of foreign peptide gene products.
                                                                                                                                                                                                                                                                           Oligonucleotide used for synthesis of MBI-11 fragment.
                            34 AAATGGCCGTGGTGGCCGTGGCGTCGTAAA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 37; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MICR-) MICROLOGIX BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-CA001107.
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                                                                                                                                           AAA27291 standard; DNA; 114
                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burian J, Bartfeld D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-400086/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity: 5
Query Match:
BB:
                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200031279-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                20-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                      AAA27291;
                                                                                            RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                        This oligonucleotide was used as a template in a PCR reaction (see also AAV60909-10) to generate a DNA fragment encoding the cationic peptide MBIII (see AAW71690). The PCR product was cloned into the universal vector path-B1, which contains the R21 replication leader of RepA (see AAW71686) and 2 tandem copies of the prepro region (Hpro) of human defendint. The vector provides expression of R21-Phpro-MBIII funion in host cells. The invention provides controlled replication plasmid vectors (RAMP vectors) comprising a replication origin of a small cryptic plasmid such as pKII (see AAV58222) and a gene encoding RepA (see AAW71686). The vectors can reach very high levels of plasmid replication, but are not lethal to the host cell, and can be used to direct the high level expression of e.g. cytokines, antigens and therapeutic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Increasing plasmid copy number in a cell with the repA gene product - and an small cryptic plasmid ori sequence, useful for high level expression of e.g. cytokines, antigens or therapeutic proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MBI28; cationic peptide; plasmid pKL1; small cryptic plasmid; replication; RepA; vector; RAMP; human; MBI11; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 88 BP; 20 A; 18 C; 25 G; 25 T; 0 U; 0 Other;
       0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                            1 ileLeuArgTrpProTrpTrpProTrpArgArgLys 12
                                                                                                                                                                                                    41 ATTCTGCGTTGGCCGTGGCGTGGCGTGGCGTAAA 76
  Conservative:
Mismatches:
Indels:
                                                                                                                   US-09-444-281-36 (1-12) x AAA27294 (1-151)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 16; Page 57; 82pp; English.
                                                                                                                                                                                                                                                                                                  AAV60908 standard; DNA; 88 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-CA000214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0040722P.
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA fragment encoding MBI11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.399
75.00
100.00%
90.00%
87.21%
  100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-531571/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burian J, Kay WW;
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BURI/) BURIAN J.
(KAYW/) KAY W W.
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14-MAR-1997;

16-MAR-1998;

24-SEP-1998.

WO9841636-A2.

Homo sapiens

Synthetic

11-JAN-1999

AAV60908;

AAV60908 RESULT

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Seguence 114 BP; 25 A; 26 C; 30 G; 33 T; 0 U; 0 Other,
                                     Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                  Indels:
                                                                                                                          US-09-444-281-36 (1-12) x AAA27291 (1-114)
                                                                                                                                                                                                                            Вb.
                                                                                                                                                                                                                            AAI72481 standard; cDNA; 68
                                    0.523
75.00
100.00%
90.00%
87.21%
                                                                                                                                                                                                                                                                             16-MAY-2002 (first entry)
                                                                                                                                                                                                                                                    AAI72481;
                                                                                                                                                                                                                AAI72481
ID AAI7
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US-09-444-281-36 (1-12) x AAV60908 (1-88)

Query Match:

Alignment Scores:

Pred. No.:

Key

cDNA derived from C-terminus of ubiquitin.

Recursive ensemble mutagenesis; REM; cell viability; optical signal; high-throughput screening; antimicrobial compound; antibiotic; ss.

셤

AAV83788 standard; DNA; 39

(first entry)

19-MAR-1999

AAV83788;

US-09-444-281-36 (1-12) x AAI72481 (1-68)

Synthetic.

/transl_except= pos:28. .30, aa:Trp /note= "No start codon given" location/Qualifiers 1. .60 /*tag= a /partial

WO200206517-A2.

24-JAN-2002.

19-JUL-2001; 2001WO-US023004

19-JUL-2000; 2000US-0219179P

(KAIR-) KAIROS SCI INC.

Youvan DC; Bylina EJ, Coleman WJ,

2002-179801/23. WPI; 2002-179801, P-PSDB; AAB47907 Screening compounds affecting cell viability e.g. for identifying antimicrobial compounds, comprises determining if induced transformed cell colonies have a desired signal when contacted with a viability

Disclosure; Fig 6; 56pp; English.

This sequence is derived from the C-terminus of ubiquitin and represents the cloning region. SacII-BgIII cassettes can be used for inserting antimicrobial peptide sequences into this region. This sequence may be used to form the recursive ensemble mutagenesis (REW) cassette of the invention. The cassette may be used in the method of the invention for determining whether a compound affects cell viability by: (a) exposing colonies of cells (CC) on a support surface to inducing conditions, where the cells have been transformed with an expression library encoding condidate compounds; (b) contacting CC with a viability indicator that produces an optical signal indicative of cell viability; and (c) determining if a colony has a desired optical signal. The method is useful for determining whether a compound affects cell viability; and (c) determining if a colony has a desired optical signal. The method is useful for high-throughput screening to identify antimicrobial compounds are useful in the pharmaceutical industry, and provide an additional new class of and in drug discovery. The antimicrobial compounds are useful in the pharmaceutical industry, and provide an additional new class of antimicrobial activity, for distinguishing dead cells (expressing active sequences) from living cells (expressing inactive or library for antimicrobial activity, for distinguishing dead cells sequences, including highly potent molecules, resulting in a large number cof new antimicrobial lead compounds that are active against a broad range of bacteria or other microcyganisms, and for screening all types of antibiotic compounds, including libraries of low molecular weight molecules produced by metabolic engineering and artificial synthesized contains in solid-phase arrays

Sequence 68 BP; 11 A; 18 C; 19 G; 20 T; 0 U; 0 Other;

Alignment Scores:

00 00 00 00

Length:
Matches:
Conservative:
Mismatches:
Indels:

0.398 74.00 100.00% 90.00% 86.05%

Percent Similarity:
Best Local Similarity:
Query Match:

Gaps:

39

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The invention relates to mass production of antimicrobial peptides. The method comprises constructing a fusion gene containing a first gene encoding a negatively charged acidic peptide having at least two cysteine residues, and a second gene encoding a positively charged basic antimicrobial peptide. A host maicroorganism is transformed with a vector containing the fusion gene and then cultured. The expressed antimicrobial peptides in recombinant microorganisms. The inhibitory office of the expressed antimicrobial peptide upon the growth of the host effect of the expressed antimicrobial peptide upon the growth of the host concordanism is considerably reduced by fusing it to the acidic peptide. Therefore, the use of the fusion gene provides an economic, recombinant calternative of mass producing antimicrobial peptides, which overcomes the disadvantages of low-productivity and poor economy, previously crepresents the DNA encoding an antimicrobial peptide Indolicidin. This can be used along with the acidic peptide Guamerin gene in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New method for mass production of antimicrobial peptides - by constructing fusion genes comprising acidic and antimicrobial peptide genes and transforming host with vector containing these.
                                                                                                                                                                                                                                                            /*tag= a
/note= "the start and stop codons are not indicated"
                                                                                                                 Antimicrobial; fusion; acidic peptide; recombinant; microorganism; guamerin; basic peptide; Indolicidin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 39 BP; 4 A; 10 C; 16 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim JH, Hong S, Lee H;
                                                                                    Antimicrobial peptide Indolicidin encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SAMY-) SAMYANG GENEX CORP. (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.
                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 6; Page 18; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                             98WO-KR000132.
                                                                                                                                                                                                                                                                                                                                                                                                                 97KR-00021312
                                                                                                                                                                                                                                                                                                                                                                                                                                98KR-00013372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lee JH, Kang MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-059844/05.
P-PSDB; AAW87609.
                                                                                                                                                                                                                                                                                                              WO9854336-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                               28-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                  09-APR-1998;
                                                                                                                                                                                                                                                                                                                                               03-DEC-1998.
                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim S,
                                                                                                                                                                                           Bos sp
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70.00 100.00% 88.89% 81.40%

Similarity: cal Similarity:

Percent Sim Best Local

Score:

Query Match

AAZ29389 standard; DNA; 47

AAZ29389

RESULT

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(first entry)

29-FEB-2000

AAZ29389;

purF gene; fusion food industry; ss.

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New DNA constructs useful for mass production of antimicrobial peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a chemically synthesised PCR primer which was used to synthesise a gene encoding antimicrobial peptide Indolicidin. antimicrobial peptide gene is used in a DNA construct that comprises entire, partial or a derivative of purF gene (glutamine pyrophosphoribosyl pyrophosphate amidotransferase gene). The DNA construct allows mass production of the antimicrobial peptide in microbial hosts without killing the host cells. The antimicrobial peptides are useful commercially in the pharmaceutical and food
                                                                                                                                                                           PCR primer-16 for synthesis of antimicrobial peptide Indolicidin gene.
                                                                                                                                                                                                          PCR primer; anti-microbial peptide; Indolicidin gene; DNA construct; glutamine pyrophosphoribosyl pyrophosphate amidotransferase gene; purF gene; flexion peptide; mass production; pharmaceutical industry; food industry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hong SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 47 BP; 12 A; 18 C; 10 G; 7 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
10
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0
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Park SH, Lee JW,
   17 AAATGGCCGTGGTGGCCGTGGCGTCGT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ArgirpProTrpTrpProTrpArgArg 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 AAATGGCCGTGGTGGCCGTGGCGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-444-281-36 (1-12) x AAZ29390 (1-47)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 13; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          99WO-KR000282.
                                                                                                                                                                                                                                                                                                                                                                                                                                             98KR-00022117.
99KR-00017920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SAMY-) SAMYANG GENEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.795
70.00
100.00%
88.89%
81.40%
                                                                    AAZ29390 standard; DNA; 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim JH, Kang MH, Lee J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL60414 standard; DNA; 47
                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in microorganism hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-097542/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                      WO9964611-A1.
                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-1999;
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                                                                                                                                          29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                       16-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       industries
                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                         AAZ29390;
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DB:
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                                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New DNA constructs useful for mass production of antimicrobial peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is a chemically synthesised PCR primer which was used to synthesise a gene encoding antimicrobial peptide Indolicidin. antimicrobial peptide gene is used in a DNA construct that comprises entire, partial or a derivative of pur gene (glutamine pyrophosphoribosyl pyrophosphate amidotransferase gene). The DNA construct allows mass production of the antimicrobial peptide in microbial peptide in the host cells. The antimicrobial peptides are useful commercially in the pharmaceutical and food
                                                                                                                                                                                                                                                                                                                                                      PCR primer-15 for synthesis of antimicrobial peptide Indolicidin gene
                                                                                                                                                                                                                                                                                                                                                                                      PCR primer, anti-microbial peptide, Indolicidin gene; DNA construct, glutamine pyrophosphoribosyl pyrophosphate amidotransferase gene; purF gene; fusion peptide; mass production; pharmaceutical industry;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 47 BP; 6 A; 11 C; 19 G; 11 T; 0 U; 0 Other;
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Matches:
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Mismatches:
Indels:
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                                                                                                     US-09-444-281-36 (1-12) x AAV83788 (1-39)
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98KR-00022117. 99KR-00017920. 99WO-KR000282

.08-JUN-1999; 09-JUN-1998; 14-MAY-1999;

W09964611-A1 16-DEC-1999.

Synthetic.

(SAMY-) SAMYANG GENEX CORP.

in microorganism hosts.

WPI; 2000-097542/08.

Kim JH,

0.795 70.00 100.00% 88.89% 81.40%

Best Local Similarity:

Query Match:

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Percent Similarity:

Alignment Scores:

Pred. No.:

Score:

industries

The

Lee H;

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Hong SS,

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08-JUN-2001; 2001KR-00031889.
                                   08-JUN-2001; 2001KR-00031889
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                                                                                                          Hong SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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 셤
                                                                                                                                                                                                                                                                                                                                                        Gene expression system useful for mass-production of peptide antibiotics and vectors derived from microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a genetic component which mass-produces peptide antibiotics effectively from microorganisms. The genetic component consists of a first gene sequence which codes for the whole or partial purF gene or its derivative, and a second gene sequence which codes for comprises. The mass-production method of peptide antibiotics comprises the steps of; constructing an expression vector including the genetic component, transformed abacterial host cell with the vector, culturing the transformed cell to express the genetic component, and recovering the peptide antibiotics. The expression vector is selected from the group consisting of pGNX2, pGNX3, pGNX4 and pGNX5, and it has a high copy number of oxigin, strong transcription promoter and structural gene. The sequences given in records ABL60400-ABL6044 represent DNA
                                                                                                                                                                                                                                                                                       Lee JW, Park SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 47 BP; 6 A; 11 C; 19 G; 11 T; 0 U; 0 Other;
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                                       Gene expression; peptide antibiotic; purF gene; ds.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-444-281-36 (1-12) x ABL60414 (1-47)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA fragment of the invention #16.
DNA fragment of the invention #15.
                                                                                                                                                                                                                                                                                          Lee
                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 7; 56pp; Korean.
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                                                                                                                                                                                08-JUN-2001; 2001KR-00031889.
                                                                                                                                                                                                                    08-JUN-2001; 2001KR-00031889.
                                                                                                                                                                                                                                                                                        Kang MH, Kim JH,
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70.00
100.00%
88.89%
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Best Local Similarity:
                                                                                                           KR2001098973-A.
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                                                                          Unidentified
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Pred. No.:
                                                                                                                                               08-NOV-2001.
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08-NOV-2001.

ABL60415;

RESULT 11

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Query Match:

Score:

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The invention relates to a genetic component which mass-produces peptide antibiotics effectively from microorganisms. The genetic component consists of a first gene sequence which codes for the whole or partial purp gene or its derivative, and a second gene sequence which codes comprises the artistic and a second gene sequence which codes comprises the ateps of; constructing an expression vector including the comprises the transforming a bacterial host cell with the vector, culturing the transformed cell to express the genetic component, and recovering the peptide antibiotics. The expression vector is selected from the group consisting of pGNX2, pGNX3, pGNX3, and it has a companion of origin, strong transcription promoter and structural gene. The sequences given in records ABL60400-ABL60464 represent DNA sequences of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      purF gene; glutamine pyrophosphoribosyl pyrophosphate amidotransferase; purF derivative; fusion partner; antimicrobial peptide; Indolicidin; mass production; cleavage site; hydroxylamine; CNBr; DNA construct; cow; neutralise; toxicity; pharmaceutical industry; food industry; ds.
                                                                                                                               Gene expression system useful for mass-production of peptide antibiotics and vectors derived from microorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= "Indolicidin peptide"
/note= "Antimicrobial peptide used in DNA construct"
                                        Park SH;
                                        ďW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47 BP; 12 A; 18 C; 10 G; 7 T; 0 U; 0 Other;
                                          Lee
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                                        Lee JH,
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Matches:
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Gaps:
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                                        Lee HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-444-281-36 (1-12) x ABL60415 (1-47)
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                                                                                                                                                                                                    Disclosure; Page 7; 56pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
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                                        Kang MH, Kim JH,
SAMY- SAMYANG GENEX CORP.
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70.00
100.00%
88.89%
81.40%
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Inhibiting growth of sulfate-reducing bacteria using other bacteria,
Kim JH,
                                                                                                                                                                                                                                                             0.902
70.00
100.00%
88.89%
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                                                                                                                                                                                                                                                                                                    81.40%
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                  WPI; 2002-301977/34.
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Kang MH,
                                                                                                                                                                                                                                                                                            Best Local Similarity:
                            P-PSDB; ABB81940
                                                                                                                                                                                                                                                                                 Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus sp.
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Hong SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wood TK,
                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ40246;
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                      The present DNA sequence encodes an antimicrobial peptide, Indolicidin derived from cow, Bos taurus. It is used along with a derivative of pure gene sequence that functions as a fusion partner. A DNA construct that comprises, this antimicrobial peptide encoding sequence and the entire, partial or derivative of pure gene, is used for mass production of the antimicrobial peptide in microorganisms without killing the host cells. Use of the pure gene derivative sequence, neutralises the toxicity of the antimicrobial peptides against the host microorganism. The antimicrobial peptides are useful commercially in the pharmaceutical and food
                                                                                                       New DNA constructs useful for mass production of antimicrobial peptides
                                                         Ë
                                                          Lee
                                                         Hong SS,
                                                                                                                                                                                                                                                               Sequence 53. BP; 8 A; 12 C; 20 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene expression; peptide antibiotic; purF gene; ds.
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Conservative:
Mismatches:
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/note= "no start codon present"
                                                       Lee JW,
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                                                                                                                                                                                                                                                                                                                                                              US-09-444-281-36 (1-12) x AAZ29364 (1-53)
                                                         Park SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA fragment of the invention #44.
                                                                                                                                    Claim 1; Fig 1; 67pp; English.
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         98KR-00022117.
99KR-00017920.
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                                    (SAMY-) SAMYANG GENEX CORP.
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/*tag= a
                                                       Kang MH, Lee J,
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                                                                                                                                                                                                                                                                                                                                  81.40%
                                                                                                                  microorganism hosts.
                                                                          WPI; 2000-097542/08.
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Best Local Similarity:
                                                                                    P-PSDB; AAY44324
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         09-JUN-1998;
14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                 Alignment Scores:
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                                                                                                                                                                                                                                              industries
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                                                         Kim JH,
                                                                                                                                                                                                                                                                                                                                  Query Match:
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The invention relates to a genetic component which mass-produces peptide antibiotics effectively from microorganisms. The genetic component consists of a first gene sequence which codes for the whole or partial purp gene or its derivative, and a second gene sequence which codes comprises the artibiotics. The mass-production method of peptide antibiotics component, transforming an expression vector including the comprises the steps of; constructing an expression vector including the cuentic component, transformed cell to express the genetic component, and recovering the preptide antibiotics. The expression vector is selected from the group consisting of polNX, poNX, poNX, and polNX, and it has a component which component is a prompt of polNX, poNX, poNX, and polNX, and it has a component of prigin, strong transcription promoter and structural gene. The sequences given in records ABL60400-ABL60464 represent DNA components.
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                                                                                                                                                                   expression system useful for mass-production of peptide antibiotics
   SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide for cloning indolicidin peptide coding sequence.
   Park
Lee JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 53 BP; 8 A; 12 C; 20 G; 13 T; 0 U; 0 Other;
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Mismatches:
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                                                                                                                                                                                                      and vectors derived from microorganisms.
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   Lee HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-444-281-36 (1-12) x ABL60445 (1-53)
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                                                                                                                                                                                                                                                                      Disclosure; Page 17; 56pp; Korean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-US009675.
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The patent discloses crosslinked analogs of indolicidin (Indol 1-13)

which is a naturally occurring peptide isolated from bovine neutrophils
and has antimicrobial activity. The crosslinked indolicidin (X-
indolicidin) analogs are stable and have antimicrobial activity against
crosslinks coli and Salmonella typhimurium), yeasts and fungi (e.g.
Candida albicans, Cryptococcus neoformans), protozo (e.g. Giardia
candida albicans, Cryptococcus neoformans), protozo (e.g. Giardia
species and Acanthamoeba species), and viruses (e.g. HIV-1). They can be
crossling or inhibiting the growth or survival of microorganisms
in an environment e.g. a food or food product, a solution, an inanimate
colject comprising a purface, or a mammal. The present sequence is a DNA
combinant construct for the expression of Indol-homoserine (Hse)
recombinant construct for the expression of Indol-homoserine (Hse)
analog. The ability of Indol-Hse analog to maintain antimicrobial
cativity provides a means to produce X-indolicidin analog precursors in
                  /*tag= e
/note= "corresponds to overlap in oligonucleotides used
/note= "corresponds to overlap in oligonucleotides used
for ligation"
complement (191. .211)
/*tag= c
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                         Crosslinked indolicidin analogs with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 211 BP; 36 A; 50 C; 74 G; 51 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-444-281-36 (1-12) x AAZ49764 (1-211)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1C; Fig 1; 53pp; English.
                                                                                                                                                                                                          99WO-US011165.
                                                                                                                                                                                                                                                   98US-00099631
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70.00
100.00%
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                                                                                                                                                                                                                                                                                                                             Osapay K;
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-147133/13.
P-PSDB; AAX44668.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                   18-JUN-1998;
                                                                                                                                                                                                            20-MAY-1999;
                                                                                                                                  W09965510-Al
    misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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                                                                                                                                                                        23-DEC-1999.
                                                                            primer bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match:
  This sequence represents an oligomucleotide for cloning the non-amidated indolicidin peptide coding sequence. The invention relates to a method cor indolicidin peptide coding sequence. The invention relates to a method cor indolicidin peptide coding sequence. The invention relates to a method cor indolicidin peptide coding specuking to the indolicidin and secretes a compound (I) albe to inhibit growth of (A). The method is cused to protect metal, concrete or cement against corrosion and degradation, but (B) can also be used to protect dental implants. (B) is present in an open or closed system (e.g. water cooling tower, liquid catorage container, fuel tank, sever or drainage system etc.) or part of a bridge or other structure. The method is more effective and less capensive than known methods for inhibiting (A), and reduces the amount of toxic chemicals released. Conventional biofilms of aerobic organisms contains this. A single application of (C) lasts for a long time, and (I) are produced exactly where they are required and inhibit (A) without care produced exactly where they are required and inhibit (A) without resistance of (A) to conventional biocides, which may then be used in reduced amounts). If local damage to the biofilm occurs, the underlying resistance and is still protected by diffusion of (I) from neighbouring areas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crosslinked indolicidin analog; X-indolicidin; poly-Indol 1-13; stability; bovine neutrophil; antimicrobial; antibacterial; fungicide; protozoacide; virucide; anti-HIV; human immunodeficiency virus-1; HIV-1; gram positive bacteria; gram negative; Staphylococcus aureus; Escherichia coli; Salmonella typhimurium; yeaet; fungi; protozoa; Candida albicans; Cryptococcus neoformans; Giardia; Acanthamoeba;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "Poly-(Indol(1-13)-Met-Ala-Arg-Ile-Ala-Met)3"
/note= "encodes three copies of Indol 1-13, each
separated by Met-Ala-Arg-Ile-Ala-Met spacer sequence"
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/note= "corresponds to overlap in oligonucleotides used
for ligation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 69 BP; 14 A; 18 C; 20 G; 17 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        000188
particularly for protection of metals and concrete,
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Matches:
Conservative:
Mismatches:
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                                  Example 4; Fig 1; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAZ49764 standard; DNA; 211 BP
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Best Local Similarity:
Query Match:
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Title:

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APPLICANT: Kay, William W
TITLE OF INVENTION: REPLICATION GENES AND GENE PRODUCTS FROM
TITLE OF INVENTION: SWALL CRYPTIC PLASMIDS AND METHODS FOR CONSTRUCTING
TITLE OF INVENTION: CONTROLLED-REPLICATION PLASMID VECTORS
NUMBER OF SEQUENCES: 52
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TO Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/09/042,071
FILING DATE: 13-MAR-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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US-09-439-313-183
US-09-352-616A-183
US-09-232-149A-183
US-09-159-812-183
US-09-118-554-59
US-09-118-627-59
US-09-602-877A-59
US-09-020-956-82
US-09-030-607-82
US-09-439-313-82
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US-09-159-812-82
US-09-636-215-82
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US-09-685-166A-183
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US-09-115-453-82
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US-09-020-956-73
US-09-030-607-73
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US-09-688-489-183
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US-09-636-215-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33,963
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: McMasters, David D. REGISTRATION NUMBER: 33,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206) 682-631
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: SEED and E
STREET: 6300 Columbia
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Seattle
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STATE:
NAME:
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 29, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 38, Appl
Sequence 5, Appli
Sequence 5, Appli
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9298, Ap
9281, Ap
6, Appli
                                                                                                                               May 11, 2004, 14:02:47; Search time 46.08 Seconds (without alignments) 144.518 Million cell updates/sec
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6: /cgm2_6/ptodata/2/ina/PCTUS_COMB.Beq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                              nucleic search, using frame_plus_p2n model
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US-09-23-180-29
US-09-282-277-1
US-09-039-631A-11
US-09-416-481A-38
US-09-525-741-5
US-09-637-751-5
US-09-66-422-5
US-09-252-991A-9269
US-09-252-991A-9269
US-09-252-991A-9261
US-09-252-991A-9261
US-09-252-991A-9261
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                                                                                                                                                                                                                                                                                                                                                                                                                        682709 seqs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                  Xgapop 10.0 , Xgapext (Ygapop 10.0 , Ygapext (Ygapop 6.0 , Ygapext Delop 6.0 , Delext
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Maximum DB seq length: 200000000
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Score

Result

Database :

75 70 70 70 70 70 63 63

App

SENERAL INFORMATION:

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APPLICANT: Kang, with Hyung
APPLICANT: Kang, with Hyung
APPLICANT: Kang, with Hyung
APPLICANT: Kim, Jeong Hyun
APPLICANT: Lee, Hyun-Soo
APPLICANT: Lee, Hyun-Soo
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
APPLICANT: Korea Advanced Institute of Science and Technology
ITILE OF INVENTION: METHOD FOR MASS PRODUCTION OF
ITILE OF INVENTION: ANTIMICROBIAL PEPTIDE
FILE REPREMENCE: 6181/06135
CURRENT APPLICATION NUMBER: BC7/KR98/00132
PRIOR PELLING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: RX 13372/1998
PRIOR PLING DATE: 1998-05-28
PRIOR PLING DATE: 1998-04-09
PRIOR PLING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 36
SOOTWARE: FastSEQ for Windows Version 3.0
IENGIN: NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: DNA sequence deduced from Indolicidin peptide OTHER INFORMATION: sequence based on codon usage of E. coli
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6 0 0 0 0
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Matches:
Conservative:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-444-281-36 (1-12) x US-09-230-180-29 (1-39)
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Matches:
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                                                                                                                                                                                                                                                                                                               34 AAATGGCCGTGGTGGCCGTGGCGTCGTAAA 63
                                                                                                                                                                                                      Indels:
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/09230180 Patent No. 6183992 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/09282277; Patent No. 6630197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                            0.129
75.00
100.00%
90.00%
87.21%
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70.00
100.00%
88.89%
81.40%
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Lee, Jae Hyun
Kang, Min Hyung
Kim, Jeong Hyun
Hong, Seung-Suh
Lee, Hyun-Soo
LENGTH: 88 base pairs
                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-042-071-49
                                                                                                                                                    Percent Similarity: 1
Best Local Similarity: 9
Query Match: 8
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                           Alignment Scores:
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US-09-282-277-1
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APPLICANT:
                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                              RESULT 2
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APPLICANT: Wood, Thomas K.
APPLICANT: Wood, Thomas K.
APPLICANT: Jayaraman, Arul
APPLICANT: Jayaraman, Arul
APPLICANT: Jayaraman, Arul
APPLICANT: Earthman, James C.
TTTLE OF INVENTION: Inhibition of Sulfate-Reducing-Bacteria-Mediated
TITLE OF INVENTION: Degradation Using Bacteria Which Secrete Antimicrobials
TITLE OF INVENTION: Degradation Using Bacteria Which Secrete Antimicrobials
FILE REPERRENCE: 02307E-08591008
CURRENT PILING DAFE: 1999-03-31
EARLIER APPLICATION NUMBER: US 09/074,037
EARLIER FILING DAFE: 1998-05-06
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description of Artificial Sequence:oligonucleotide used for cloning indolicidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/0909931A

Sequence 11, Application US/0909931A

Sequence 11, Application US/0909931A

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Osapay, Klara

TITLE OF INVENTION: Crosslink-Stabilized Indolicidin Analogs

FILE REFERENCE: P-UC 3050

CURRENT APPLICATION NUMBER: US/09/099,631A

CURRENT FILING DATE: 1998-06-18

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 11

LENGING: LENGING CONTRACT OF THE CONTRACT O
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COCATION: (8)...(196)
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: Construct
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
Gaps:
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Matches:
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70.00
100.00%
88.89%
81.40%
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100.00%
88.89%
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Best Local Similarity:
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COTHER INFORMATION:
US-09-282-277-1
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Pred. No.:
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TELEFAX: 650-463-8400
TELEX:
INFORMATION FOR SEQ ID NO:
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Patent No. 6033895
GENERAL INFORMATION: 6033895
GENERAL INFORMATION: BARGER, STEPHEN
APPLICANT: GARGER, STEPHEN
APPLICANT: MCCULLOCH, MICHAEL
APPLICANT: TURBEN, THOWAS
TITLE OF INVENTION: PROCESS FOR ISOLATING AND
TITLE OF INVENTION: PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT
TITLE OF INVENTION: SOURCES
                                            AGOUNT >
US-09-416-401A-30

| Sequence 38, Application US/09416401A
| Sequence 38, Application US/09416401A
| Patent No. 6524565
| GENERAL INFORMATION:
| APPLICANT: Selsted, Michael E.
| TITLE OF INVENTION: Indolicidin Analogs and Methods of Using Same |
| FILE REFERENCE: P-UC 3794
| CURRENT APPLICATION NUMBER: US/09/416,481A
| CURRENT APPLICATION NUMBER: US/09/416,481A
| CURRENT APPLICATION NUMBER: US/09/416,27
| PRIOR PLIING DATE: 1998-10-12
| PRIOR FILING DATE: 1998-16-12
| NUMBER OF SEQ ID NOS: 39
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 38
| LENGH' = 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: construct
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Matches:
Conservative:
Mismatches:
Indels:
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SOFTWARE: FastSEQ for Windows Version 2.0
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STREET: 1299 Pennsylvania Avenue N.W.
38 AAATGGCCGTGGTGGCCGTGGCGTCGT 64
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APPLICATION UNMER: US/09/259,741
FILING DATE: February 25, 1999
CLASSIFICATION:
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APPLICATION NUMBER: 09/037,751
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
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88.89%
81.40%
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (8)..(196)
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-416-481A-38
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US-09-259-741-5
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APPLICANT: GARGER, STEPHEN
APPLICANT: GARGER, BARRY
APPLICANT: MCCULLOCH, MICHAEL
APPLICANT: MCCULLOCH, MICHAEL
APPLICANT: THORMS
TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
TITLE OF INVENTION: PROM PLANT SOURCES
TITLE OF INVENTION: FROM PLANT SOURCES
TITLE OF INVENTION: FROM PLANT SOURCES
CORRESPONDENCE S.5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWYER'S SIMON
STREET: 1299 Pennsylvania Avenue N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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MEDIUM TYPE: Diskette
COMFUTER: IBM COMPATIBLE
OWNUTER: IBM COMPATIBLE
OWNTARE: FastSEC for Windows Version 2.0
SOFWARE: FastSEC for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 10-MAR-1998
CLASSIFICATION:
PHICR APPLICATION:
APPLICATION:
APPLICATION:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-444-281-36 (1-12) x US-09-259-741-5 (1-6446)
ATTORNEY TAGRAT INFORMATION:
NAME: Halluin, Albert P
REGISTRATION NUMBER: 25,277
TERERENCE/DOCKET UNMBER: 00801.0140.US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00801.0140.999
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ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P
REGISTRATION NUMBER: 25,277
REFERENCE/DOCKET NUMBER: 0080
TELECOMMUNICATION:
TELEPHONE: 650-463-8109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09037751
Patent No. 6037456
                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 6446 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                Genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       39.8
70.00
100.00%
88.89%
81.40%
                                                                                                                                                              TELEFAX: 650-463-8400
                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown;
MOLECULE TYPE: Genor
US-09-259-741-5
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Best Local Similarity:
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100.00%
88.89%
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100.00%
73.26%
                                                                                      81.40%
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Query Match:
DB:
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Best Local Similarity:
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                                              Percent Similarity:
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      Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TURPEN, THOMAS
TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
FROM PLANT SOURCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

COUNTRY: USA

COMPUTER READABLE FORM:

MEDLUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSR for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/466,422

FILING DATE: 17-Dec-1999

CLASSIFICATION: dhknown>
PRIOR APPLICATION: dhknown>
PRIOR APPLICATION: Albknown>
APPLICATION NUMBER: 09/037,751

FILING DATE: CLAKNOWN>
APPLICATION NUMBER: 09/037,751

FILING DATE: CLAKNOWN>
APPLICATION NUMBER: 25,277

REGISTRATION NUMBER: 25,277

RESPERRENCE/DOCKET NUMBER: 25,277

TELEBRONGINICATION INFORMATION:

TELEBRONGINICATION INFORMATION:
                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWIEV & SIMON
STREET: 1299 Pennsylvania Avenue N.W.
CITY: Nashington
                                                                                                                                                                                                                                                                                                                                          US-09-444-281-36 (1-12) x US-09-037-751-5 (1-6446)
                                                                                                                                                                                                                                                                              Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: Genomic RNA
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESUL: 0
US-09-466-422-5
; Sequence 5, Application US/09466422
; Patent No. 6303779
; GENERAL INFORMATION:
; APPLICANT: GARGER, STEPHEN
; HOLTZ, R. BARRY
; MCCLILOCH, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 6446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650-463-8400
TELEX: <Unknown>
SEQUENCE CHARACTERISTICS:
LENGTH: 6446 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPDLOGY: unknown
MOLECULE TYPE: Genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          39.8
70.00
100.00%
88.89%
81.40%
                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                      Alignment Scores:
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                                                                                                                              US-09-037-751-5
                                                                                                                                                                                                                                                                              Query Match:
DB:
                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                  Score:
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Alignment Scores:

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US-09-252-991A-9998/c
i Sequence 9298, Application US/09252991A
Fatent No. 6551795
GENERAL INFORMATION:
ATTLE OF INVENTION: WICHEL ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
SEQ ID NO 9298
NUMBER OF SEQ ID NOS: 33142
MUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196 136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9269
LENGTH: 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1362
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Matches:
Conservative:
Mismatches:
Indels:
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Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                              US-09-444-281-36 (1-12) x US-09-466-422-5 (1-6446)
                                                                                                      Indels:
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                                                                                                                                                                                                                              3 ArgirpProTrpTrpProTrpArgArg 11
                                                                                                                                                                                                                                                                                                                                                                               Sequence 9269, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
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Pred. No.:
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RESULT 13
US-09-108-554-59
Sequence 59, Application US/09118554A
Patent No. 6365348
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: R.W. Jianghun
TITLE OF INVENTION: COMPOUNDS FOR DIAGNOSIS OF BREAST CANCER AND
TITLE OF INVENTION: WETHOUS FOR THEIR USE
FILE REFERENCE: 21012.4501
CURRENT APPLICATION NUMBER: US/09/118,554A
CURRENT FILING DATE: 1990-07-17
EARLIER APPLICATION NUMBER: 08/988,255
RARLIER FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 67
SEQ ID NO 59
SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
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Conservative:
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Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,035
FILING DATE: 28-UUL-1997
CLASSIFICATION: 800
RAIDS APPLICATION DATA:
APPLICATION NUMBER: GB 9414622.2
FILING DATE: 20-UUL-1994
PRIDR APPLICATION NUMBER: GB95/01678
FILING DATE: 17-UUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patticia.
REFERENCE/DOCKET NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:132
TELEPHONE: 713.787.1440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IleLeuArgTrpProTrpFroTrp 9
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                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 758 base pairs TYPE: mucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.00
88.89%
77.78%
70.93%
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59.00
87.50%
87.50%
68.60%
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US-09-118-554-59
                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-793-035-6
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                        APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APRUGICAS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-18

PRIOR FILING DATE: 1998-07-27

NUMBER: OF SEQ ID NOS: 33142

LENGTH: 1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Squence 6, Application US/08793035
Patent No. 6011201
GENERAL INFORMATION:
APPLICANT: Slabas, Antoni R.
APPLICANT: Milte, Andrew
APPLICANT: Chase, Dianne
APPLICANT: Fentem, Phillip A.
TITLE OF INVENTION: B-Ketcoacyl ACP Reductase Genes From
     00000
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COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROPER PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                          US-09-444-281-36 (1-12) x US-09-252-991A-9298 (1-1362)
 Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                       US-09-252-991A-9281
; Sequence 9281, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          992 rédecerregregeceraded 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                        623 TGGCCCTGGTGCCCTGGCGA 603
                                                                                                                                                4 TrpProTrpTrpProTrpArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 TrpProTrpTrpProTrpArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
63.00
100.00%
100.00%
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63.00
100.00%
100.00%
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           Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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Sequence 59, Application US/09118627A,
Patent No. 6379951
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF BREAST CANCER
TITLE OF INVENTION: AND METHODS FOR THEIR USE;
FILE REFERENCE: 210121.446C1
CURRENT APPLICATION WUBBER: US/09/118,627A
CURRENT FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 67
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 59
LENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCORNATION:

APPLICANT: Reed, Steven G.
APPLICANT: Ru, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFREENT APPLICATION: UNMERR: US/09/602,877R
CURRENT APPLICATION NUMBER: US/09/602,877R
CURRENT FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSEQ for Windows Version 3.0
SET 382
IENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-444-281-36 (1-12) x US-09-118-627-59 (1-382)
155 CTTCGCTGGCCTTGGTGGAGCTGG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 CTTCGCTGGCCTTGGTGGAGCTGG 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 LeuArgTrpProTrpTrpProTrp 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-602-877A-59
; Sequence 59, Application US/09602877A
; Patent No. 6432707
                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.6
59.00
87.50%
87.50%
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59.00
87.50%
87.50%
                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA; ORGANISM: Homo sapien US-09-118-627-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo sapien
US-09-602-877A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity: 1
Best Local Similarity: 6
Query Match: 6
DB:
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Best Local Similarity:
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                                   RESULT 14
US-09-118-627-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
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155 chrcecrecchregregacres 178

Search completed: May 11, 2004, 16:58:19

2 LeuArgTrpProTrpTrpProTrp 9

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Job time : 48.08 secs

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APPLICANT: Suleman, Dinar
TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
TITLE OF INVENTION: AMETHODS FOR PEPTIDES
FILE REFERENCE: 660081.421
CURRENT APPLICATION NUMBER: US/10/395,896
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 70
SOPTWARE: FastSEQ for Windows Version 4.0
LENGTH: 72
  16 US-10-395-896-32

16 US-10-395-896-28

16 US-10-395-896-62

16 US-10-395-896-31

16 US-10-395-896-31

16 US-10-395-896-65

16 US-10-395-896-65

16 US-10-395-896-65

19 US-09-996-52-6

10 US-09-996-52-7

11 US-10-352-773-15

12 US-10-252-773-15

13 US-10-252-773-17

13 US-10-252-773-17

14 US-10-252-773-17

15 US-10-252-773-17

16 US-10-252-773-17

17 US-10-252-773-17

18 US-10-252-773-17

19 US-09-815-242-716

19 US-09-815-242-716

19 US-09-815-242-9716

19 US-09-815-242-9716

19 US-09-815-242-9716

19 US-09-815-242-9716

19 US-09-815-242-9716

19 US-09-815-242-9716

11 US-10-359-928-17644

12 US-10-369-99-722-157

13 US-10-424-599-17642

13 US-10-425-114-30359

13 US-10-425-114-30359

13 US-10-425-114-30359

13 US-10-425-114-3031

14 US-10-425-114-3031

15 US-09-813-62-838-13208

16 US-10-282-132A-13208

16 US-10-282-132A-13208

16 US-10-245-235A-13208
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Publication No. US20030219854A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Guarna, Maria Marta
APPLICANT: Chen, Yuchen
APPLICANT: Cory, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Brinkman, Jacqui
APPLICANT: Cabralda, Jennifer
APPLICANT: Metlitskaia, Luba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 72
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2403 1
9025608
1224 1
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1825
2218
2218
412
1038
1072
8429
837
1440
1596
7333
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63
61.5
61.5
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-MODEL-frame+_p2n.model -DEV-xlh
-Q=(0912_1/10SPTO_spool)/USD9444281/runat_07052004_171139_2611/app_query.fasta_1.398
-Q=(0912_1/10SPTO_spool)/USD9444281/runat_07052004_171139_2611/app_query.fasta_1.398
-DB=Published Applications NA -QFMT=fastap -SUFFX=rnpb-MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -STRART=1 -END=-1 -MATRIX=b)csum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=1= -MODEL-LOCAL -OUTFWT=pto -NORM=ext -HEAPSIZE=500 -MINIEN=0
-MAXIEN=2000000000 -USER=USG9444281 -GCGN 1 1 271 -Grunat -07052004 171139_2611
-NCPU=6 -ICPU=3 -NO PMAAP -LAAGEQDERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGING -DEY TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOP=6 -DBLEXT=7
                                                                                                                                                                                              (without alignments)
209.334 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/NCO7_BNB_PUB_seq:*
3: /cgn2_6/ptodata/2/pubpna/NCO6_NEW_PUB_seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB_seq:*
5: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB_seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
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12: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_
                                                                                                                                                                May 11, 2004, 14:35:33 ; Search time 259.68 Seconds
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/cgn2_6/ptodata/2/pubpna/US60 NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5883172
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                        OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2941586 segs, 2264995651 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Xgapop 10.0 , Xgapext 0
Ygapop 10.0 , Ygapext C
Fgapop 6.0 , Fgapext C
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Score Match Length DB
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Sequence 23253, A Sequence 23253, A Sequence 1131, Ap Sequence 1762, A Sequence 27681, A Sequence 4367, Ap Sequence 2961, Ap Sequence 2961, Ap Sequence 13208, A Sequence 13208, A

Sequence 59, Appl Sequence 59, Appl

Description

a

Result Мо.

Database :

Sequence 17, Appl Sequence 17, Appl Sequence 53929, A Sequence 321717, Sequence 321717, Sequence 311717, Sequence 1766, Ap Sequence 1766, Ap Sequence 9716, Ap Sequence 1766, Ap Sequence 1767, Ap Sequence 1607, Ap Sequence 1764, Appl Sequence 12845, A Sequence 12845, A Sequence 12845, A Sequence 17644, Appl Sequence 1764, Appl Sequence 1778, Appl

Sequence 6, Appli Sequence 60, Appl

Sequence 29, Sequence 31, Sequence 30, Sequence 64, Sequence 65,

Sequence 62

Sequence 5, Appl.

Sequence 25, Sequence 15,

Scoring table:

Searched:

Perfect score:

Run on:

Seguence:

à

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; Sequence 31, Application US/10395896
; Publication No. US20030219854A1
                                                                                                                                                                                                                                                                    Alignment Scores:
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Pred. No.:
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US-10-395-896-31
                                                                                                                                                                        FEATURE:
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                                                                                                                                                                                                                                                                                   Pred. No.:
                                                                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                              WS-10-395-896-28

Sequence 28, Application US/10395896

Publication No. US20030219854A1

GENERAL INFORMATION:

APPLICANT: Guarna, Maria Marta

APPLICANT: Gren, Vuchen

APPLICANT: Cory, Robert

APPLICANT: Carildan, Jacohit

APPLICANT: Cabralda, Jennifer

APPLICANT: Cabralda, Jennifer

APPLICANT: Stileman, Dinar

TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED

TITLE OF INVENTION: ANTI-INFECTIVE PEPTIDES

FILE REFERENCE: 660091.421

CURRENT APPLICATION NUMBER: US/10/395,896

CURRENT FILING DATE: 2003-03-21

NUMBER OF SEQ ID NOS: 70

SEQ ID NO 28

LIGHTH: LIGHTHE PARESEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 28

LIGHTH: LIGHTHE PARESEQ FOR WINDOWS VERSION 4.0
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APPLICANT: Guarna, Maria Marta
APPLICANT: Guarna, Maria Marta
APPLICANT: Chen, Yuchen
APPLICANT: Chen, Yuchen
APPLICANT: Cary, Robert
APPLICANT: Cabralda, Jennifer
APPLICANT: Cabralda, Jennifer
APPLICANT: Suleman, Dinar
APPLICANT: Suleman, Dinar
TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
TITLE OF INVENTION: ANTI-INFECTIVE PEPTIDES
                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                     5 ATTCTGCGTTGGCCGTGGCGTGGCGTGGCGTAA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                         US-09-444-281-36 (1-12) x US-10-395-896-32 (1-72)
                 ; OTHER INFORMATION: Exemplary "template"
US-10-395-896-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Exemplary "template"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                       0.00445
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
                                                                        Alignment Scores:
Pred. No.:
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; FEATURE:
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) OTHER INFORMATION: Nucleic acid template encoding anti-infective
; OTHER INFORMATION: peptide 11B7 and anionic spacer peptide S11 or S12
US-10-395-896-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/10395896
| Sequence 29, Application US/10395896
| Publication No. US20030219854A1
| GENERAL INFORMATION:
| APPLICANT: Ghen, Waria Marta APPLICANT: Cory, Robert
| APPLICANT: Cory, Robert
| APPLICANT: Cabralda, Jennikann, Jacqui
| APPLICANT: Brinkman, Jacqui
| APPLICANT: Brinkman, Juba APPLICANT: Mellitskaia, Luba
| APPLICANT: Mellitskaia, Luba
| APPLICANT: Mellitskaia, Luba
| APPLICANT: Mellitskaia, Suleman, Dinar
| TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
| TITLE OF INVENTION: MATI-INPECTIVE PEPTIDES
| TITLE REFERENCE: 660081.421
| CURRENT APPLICATION NUMBER: US/10/395,896
| CURRENT APPLICATION NUMBER: US/10/395,896
| CURRENT FILING DATE: 2003-021
| NUMBER OF SEQ ID NOS: 70
| SEQ ID NO 29
| LENTH: 123
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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FILE REFERENCE: 660081.421
CURRENT APPLICATION NUMBER: US/10/395,896
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 62
LENGTH: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
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                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity:
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Best Local Similarity:
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Sequence 30, Application US/10395896
| Sequence 30, Application US/10395896
| Publication No. US20030219854A1
| GENERAL INFORMATION:
| APPLICANT: Guarna, Maria Marta
| APPLICANT: Cory, Robert
| APPLICANT: Cory, Robert
| APPLICANT: Cabralda, Jennifer APPLICANT: Cabralda, Jennifer APPLICANT: Cabralda, Jennifer APPLICANT: ASIDHAMA: MAILENARA, DUBA
| APPLICANT: Metlitskaia, Luba
| APPLICANT: ASIDHAMA: DIART: APPLICANT: Metlitskaia, Duba
| APPLICANT: Metlitskaia, ENGROUCING MODIFIED
| TITLE OF INVENTION: ANTI-INFECTIVE PERTIDES
| TITLE OF INVENTION: ANTI-INFECTIVE PERTIDES
| TITLE OF INVENTION: ANTI-INFECTIVE PERTIDES
| CURRENT FILING DATE: 2003-03-21
| NUMBER OF SEQ ID NOS: 70
| SEQ ID NO 30
| LENGTH::166
APPLICANT: Guerral Maria Marta
APPLICANT: Chen, Yuchen
APPLICANT: Chen, Yuchen
APPLICANT: Cory, Robert
APPLICANT: Cabralda, Jacqui
APPLICANT: Cabralda, Jennifer
APPLICANT: Cabralda, Jennifer
APPLICANT: Cabralda, Jennifer
APPLICANT: Suleman, Dinar
TITLE OF INVENTION: METHODS FOR PRODUCING MODIFIED
FITLE OF INVENTION: MATHODS FOR PROPULING
FILE OF INVENTION: ANTI-INFECTIVE PEPTIDES
CURRENT APPLICANTON NUMBER: US/10/395, 896
CURRENT FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Fast-SEQ for Windows Version 4.0
FERMIND 31
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Exemplary "template"
US-10-395-896-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Exemplary "template"
US-10-395-896-30
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-10-395-896-30
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) OTHER INFORMATION: Nucleic acid template encoding precursor peptide ; OTHER INFORMATION: 11B25 and anionic spacer peptide S21. US-10-395-896-64
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Publication No. US20030219854A1
GENERAL INFORMATION:
APPLICANT: Gurna, Maria Marta
APPLICANT: Chen, Yuchen
APPLICANT: Cry, Robert
APPLICANT: Brinkman, Jacqui
APPLICANT: Brinkman, Jacqui
APPLICANT: Brinkman, Dinar
APPLICANT: Brinkman, Dinar
APPLICANT: APPLICANT: Mellitskaia, Luba
APPLICANT: Mellits
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                                               19 ATTCTGCGTTGGCCGTGGCCGTGGCGTCGCAAA 54
1 IleLeuArgTrpProTrpTrpProTrpArgArgLys 12
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 IleLeuArgTrpProTrpTrpProTrpArgArg 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-444-281-36 (1-12) x US-10-395-896-64 (1-114)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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100.00%
100.00%
94.19%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                      US-10-395-896-64
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LENGTH: 114
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; Sequence 6, Application US/09909652
; Patent No. US200202537A1
general invormation:
; APPLICANT: Kairos Scientific, Inc.
; APPLICANT: Alina, Edward J.
; APPLICANT: Ocleman, William J.
; APPLICANT: Coleman, William J.
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR GENERATING
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR GENERATING
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR GENERATING
; CURRENT APPLICATION NUMBER: US/09/909,652
; CURRENT APPLICATION NUMBER: US 60/219,179
; RIOR APPLICATION NUMBER: US 60/219,179
; RIOR PAPLICATION NUMBER: US 60/219,179
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Nucleic acid encoding ubiquitin indolicidin fusion OTHER INFORMATION: protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence (60, Application US/10076816

Publication No. US20030056244A1

GENERAL INFORMATION:

APPLICANT: Hoang Ning

APPLICANT: Hagie, Frank E.

TITLE OF INVENTION: Feed Additive Compositions and Methods

TITLE OF INVENTION: Feed Additive Compositions and Methods

CURRENT APPLICATION NUMBER: US/10/076,816

CURRENT FILING DATE: 2002-02-14

PRIOR PELICATION UNMBER: US 60/269,188

PRIOR PAPLICATION NUMBER: US 09/847,232

PRIOR PELING DATE: 2001-05-02
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Matches:
Conservative:
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Matches:
Conservative:
                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                85 ATTCTGCGTTGGCCGTGGCCGTGGCGTCGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
Indels:
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                                                                                                                                                                                                               US-09-444-281-36 (1-12) x US-10-395-896-65 (1-114)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 TTGAAATGGCCTTGGTGGCCTTGGCGTCGC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                            0.0278
81.00
100.00%
100.00%
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74.00
100.00%
90.00%
86.05%
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                                                                                                    Percent Similarity:
Best Local Similarity:
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                                            Alignment Scores:
US-10-395-896-65
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DB:
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DB:
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SOLUBLE PROTEINS AND PEPTIDES
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURBUT APPLICATION DATA:
APPLICATION NUMBER: US/09/962,527
FILING DATE: 24-Sep-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION NUMBER: US/037,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: GARGER, STEPHEN
HOLTZ, R. BARRY
MCCHLLOCH, MICHAEL
TURPEN, THOMAS
TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 00801.0140.999 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.
CIIY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-444-281-36 (1-12) x US-10-076-816-60 (1-550)
PRIOR APPLICATION NUMBER: US 60/266,929
PRIOR PLILING DATE: 2001-02-06
PRIOR PLICATION NUMBER: US 60/201,182
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 60
IENGTH: 550
TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM PLANT SOURCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415 AAATGGCCATGGTGCCTTGGCGAGA 441
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ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P
REGISTRATION NUMBER: 25,277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PURIFYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-962-527-5
; Sequence 5, Application US/09962527
; Publication No. US20030049813A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 650-463-8109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 6446 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650-463-8400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown MOLECULE TYPE: Genomic RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                  100.00%
88.89%
81.40%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: DC
COUNTRY: USA
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                            Alignment Scores:
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RESULT 15
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APPLICANT: INTENCENT. INTENCENT.
APPLICANT: LI, QUNIGSHUN
APPLICANT: LAWRENCE, CHRISTOPHER
APPLICANT: LAWRENCE, CHRISTOPHER
APPLICANT: LAWRENCE, CHRISTOPHER
TITLE OF INVENTION: DEGRADATION
FILE REFERENCE: INTENLINK 3.0-003
CURRENT APPLICATION NUMBER: 60/105,23
PRIOR APPLICATION NUMBER: 60/106,373
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: 60/106,573
PRIOR FILING DATE: 1998-11-02
SOFTWARE: PATENTING DATE: 1998-11-02
SOFTWARE: PATENTING DATE: 1998-11-02
SOFTWARE: PATENTING DATE: 1998-11-02
SEQ ID NO 25
LENGHARE: PATENTING VAIL STANDARD SEQ ID NO 25
LENGHARE: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA PCRIL,
OTHER INFORMATION: CONSTRUCT
US-10-222-773-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, Application US/10252773

Publication No. US20030131383A1

GENERAL INFORMATION:
APPLICANT: EVERET, NICHOLAS P.
APPLICANT: LI, OUNIGSHUN
APPLICANT: LAWRENCE, CHRISTOPHER
TITLE OF INVENTION: PEFTIDES WITH ENHANCED STABILITY TO PROTEASE
TITLE OF INVENTION: DEGRADATION
TITLE OF INVENTION: DEGRADATION
FILE REFERENCE: INTERLINK 3.0-003
CURRENT APPLICATION NUMBER: US/10/252,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                              Conservative:
Mismatches:
Indels:
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                                                                                      Length:
Matches:
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                                                                                                                                                                                                                                                                                                                        6213 AAGUGGCCUUGGUGGCCAUGGCGCCGA 6239
                                                                                                                                                                                                                                                                                  3 ArgTrpProTrpTrpProTrpArgArg 11
                                                                                                                                                                                                Gaps:
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-962-527-5
                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 25, Application US/10252773; Publication No. US20030131383A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                 24.2
70.00
100.00%
88.89%
81.40%
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67.00
90.00%
80.00%
77.91%
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Best Local Similarity: 6
Query Match: BB
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                                                             Alignment Scores:
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US-10-252-773-25
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                                                                                                            Score:
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Sequence 17, Application US/10252773

Sequence 17, Application US/10252773

Publication No. US2003131383A1

GENERAL INFORMATION:
APPLICANT: EVERTY, NICHOLAS P.
APPLICANT: LI, QUNICETUM USCREADER
APPLICANT: LAWRENCE, CHRISTOPHER
TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
TITLE OF INVENTION: DECRADATION
FILE REFERENCE: INTERLINK 3.0-003
CURRENT PAPLICATION NUMBER: US/10/252,773
CURRENT FILING DATE: 1998-10-30

PRIOR RILING DATE: 1998-11-02

PRIOR FILING DATE: 1998-11-02

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTY OF THE STATE STAT
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                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
FOTHER INFORMATION: Description of Artificial Sequence:
GTHER INFORMATION: Oligonucleotide
US-10-252-773-15
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/106,373
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 60/106,573
PRIOR APPLICATION NUMBER: 60/106,573
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AGATGGCCTTGGTGGCCTTGGAAA 27
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                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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65.00
100.00%
87.50%
75.58%
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65.00
100.00%
87.50%
75.58%
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Best Local Similarity:
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US-10-252-773-19/c
; Sequence 19, Application US/10252773
; Publication No. US200301313B3A1
; GENERAL INFORMATION:
; APPLICANT: LI, QUNIGSHUN
; APPLICANT: LI, QUNIGSHUN
; APPLICANT: LI, QUNIGSHUN
; APPLICANT: LAWRENCE, CHRISTOPHER
; APPLICANT: LAWRENCE, MAELOR H,
; TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
; TITLE OF INVENTION: PEPTIDES WITH ENHANCED STABILITY TO PROTEASE
; TITLE OF INVENTION: DESTADATION
; FILE REFERENCE: INTERLINK 3.0-003
; CURRENT PELLING DATE: 2002-09-373
; PRIOR FILING DATE: 1998-10-30
; PRIOR PELLOR NUMBER: 60/106,373
; PRIOR FILING DATE: 1998-11-02
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 54
; TYPE: DNA
; REATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-252-773-19
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Length:
Matches:
Conservative:
Mismatches:
Indels:

1.32 65.00 100.00% 87.50% 75.58%

> Percent Similarity: Best Local Similarity:

Score:

Query Match: DB:

Alignment Scores:

Gaps:

Search completed: May 11, 2004, 17:07:35 Job time: 262.68 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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frame_plus_p2n model OM protein - nucleic search, using May 11, 2004, 14:00:48 ; Search time 1588.8 Seconds Run on:

(without alignments)
225.545 Million cell updates/sec 27513289 seqs, 14931090276 residues Xgapop 10.0 , Xgapext (Ygapop 10.0 , Ygapext (Fgapop 6.0 , Fgapext Delop 6.0 , Delext 1 ILRWPWWPWRRK 12 US-09-444-281-36 86 **BLOSUM62** Title: Perfect score: Scoring table: Sequence: Searched:

55026578 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 200000000

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EST:* Database :

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em_gss_fun:*
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gb_gss2:* 29:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	75	7.	N.	14	4793	9395 RTWW3_
	69	Ġ.	446	9	AU198144	144 AU19814
	69	80.2	448	6	3162	8162 AU19816
	69	ď	539	14	CF326637	26637 JMT1-
	69	ď	550	₩.	CF326444	26444 JMT1
	69	ö	559	14	CF325873	5873 JMT1
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	69	ď	Н	::	BC034057	Mus
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	68	φ.	471	12	BJ475478	75478 BJ47547
	68	φ.	472	N	BJ475115	BJ475115 BJ475115
	68	œ.	472		BJ476710	76710 BJ47671
	68	Ψ.	473		AV937233	233 AV937233
	68	٠.	474	N	BJ473880	3880 BJ4738
	68	<u>.</u>	475	σ	AU089934	4
	68	۳.	æ	12	71	718
	68	Ψ.	0	12	BJ475153	5
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	68	÷	0	12	BJ475306	30
	68	œ.	206	12	BJ471761	7176
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	68	÷.	0	17	BJ471258	7125
	68	ď.	н	12	BJ469760	9169
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	68	φ.	531	12	BJ475836	75836 BJ47583
			-		1	

ALIGNMENTS

CF479395 F22 bp mRNA linear EST 08-SEP-2003 RTWW3.23 A01.gl A022 Well-watered loblolly pine roots WW3 Pinus taeda cDNA clone RTWW3.23 A01_A022 5', mRNA sequence. Pinus taeda (loblolly pine) CF479395 CF479395.1 GI:34508264 Pinus taeda RESULT 1 CF479395 LOCUS DEFINITION VERSION KEYWORDS SOURCE ORGANISM ACCESSION

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 522)

REFERENCE

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em gas mus: em gas pro:

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EST 03-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embrartophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzae; Oryza.
1 (bases 1 to 448)
Sasaki, T. and Yamamoto, K.
Wice cDNA from green shoot (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU198162 AU200 448 bp mRNA linear EST 03-APR-20 AU198162 Rice green shoot Oryza sativa (japonica cultivar-group) CDNA clone S16019, mRNA sequence.
                     Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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Matches:
Conservative:
Mismatches:
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                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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         305-8602, Japan
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                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
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DB:
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DB:
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AUTHORS
TITLE
JOURNAL
COMMENT
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                                                                                                                      FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3352"
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                                                                 An EST database from well-watered loblolly pine (Pinus taeda) roots Unpublished (2003)
Ochbrished (2003)
Cohter ESTS: RTWN3 23 A01.bl A022
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                        RMAIL: mmpratt@nga.edu
RNA prepared and library constructed by W. Walter Lorenz, School of
Forestry, University of Georgia, plant material prepared at the
Forestry, University of Florida; sequencing done in the Laboratory for
Genomics and Bioinformatics, University of Georgia. Sequence ends
have been trimmed to exclude vector and regions below Phred quality
16. Three-prime sequences are presented as their reverse complement
and have been trimmed to exclude polya.
Seq primer: JENREV (CAGGAAACAGCTAATGACC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU198144 AU202 AU198144 Rice green shoot Oryza sativa (japonica cultivar-group)
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
  Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Dean,J.,
Gebremedhin,M., Dervinis,C., Martin,T., White,T., Davis,J. and
                                                                                                                                                           Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
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Rice cDNA from green shoot (2001)
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA clone S15951, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Pinus taeda"
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Fax: 706 583 0210
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
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à a

LOCUS

RESULT 4 CF326637/c

RESULT

8 엄 VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

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Anotes "Vector: pBluescript SK(+); Site_1: EcoRI; Site_2: XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5 end with EcoRI and 3' end with XhoI site. mRNA was prepared from Arabidopsis Jasmoinate Carboxyl methyltransferase overexpression line."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JAT1--04-H09.gl AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--04-H09, mRNA
                                                                                      Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyra, Magnoliophyra, Liliopsida, Poales, Poaceae, Enrhartoideae, Oryza.

Enrhartoideae, Oryzae, Oryza.

I (bases 1 to 550)

Kim, J.S., Jun, K.M., Cheong P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzae.

Enhartoideae; Oryzae; Oryza.

I (bases I to 559)

Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Man, Y. -K. and Nahm, B. H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B. H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                                                                                                                                                                                                                                                                                   Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="14 days after germination"
| Tab host="Rs.coli SOLR"
| Alone | Lib="AttMT-overexpressing transgenic rice lambda phage cDNA library (JMT1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
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CF325873.1 GI:33800014
     CF326444.1 GI:33801141
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Oryza sativa
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CF325873/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue typin="leaf"
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/lab.bote="B..col; SORR
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end with EcoRI and 3' end with XhoI site. mRNR was
prepared from Arabidopsis Jasmoinate Carboxyl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6135
Fax: 82 31 321 6355
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JMT1--06-B08.gl AtJMT-overexpressing transgenic rice lambda phage cDNA library (JMT1) Oryza sativa cDNA clone JMT1--06-B08, mRNA
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Mismatches:
Indels:
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                                                                          3 ArgTrpProTrpTrpProTrpArgArgLys 12
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                         US-09-444-281-36 (1-12) x AU198162 (1-448)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
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Oryza sativa
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CF326444/c LOCUS DEFINITION

RESULT 5

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Pred. No.:

Score:

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CF326279

JMT1--05-K03.gl AtJMT-overexpressing transgenic rice lambda phage cDM library (JMT1) Oryza sativa cDNA clone JMT1--05-K03, mRNA
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Xhoi; GDNA was inserted into landa Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with Xhoi site. mRNA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
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Oryza sativa
Lyza sativa
Lyza sativa
Lyza sativa
Lyza sativa
Lyza sativa
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzae; Oryza.
L (basse 1 to 595)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
Stongin, KyeongJi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongJi.ac.kr.

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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzeae; Oryza.
Enthartoideae; Oryzeae; Oryza.
Enthartoideae; Oryzeae; Oryza.
Sasaki, T. and Yamamoto, K.
Sasaki, T. and Yamamoto, K.
Orpublished (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
Tel: 81-299-38-7441
                                                                                                                                                                                                                                               /tissue_type="leaf"
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Xhoi; cDNA was inserted into landa Uni-ZAP XR vector at 5'
end with EcoRI and 3' end with XhoI site, mENA was
prepared from Arabidopsis Jasmoinate Carboxyl
methyltransferase overexpression line."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU082117 578 bp mRNA linear EST 02-APR-
M082117 Rice panicle at ripening stage Oryza sativa (japonica
cultivar-group) cDNA clone E11611, mRNA sequence.
AU082117
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of Bioscience and Bioinformatics, MyongJi University Yongin, Kyeonggi, Korea 1818 81 31 31 6193 Fax: 82 31 321 6355 Fax: 82 bhnahm@ggbjo.com, bhnahm@bio.myongji.ac.kr.
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Matches:
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Mus musculus (Logic Modata; Craniata; Vertebrata; Euteleostomi; Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Enkaryota; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. B. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. S. NTH-MGC http://mgc.nci.nih.gov/.

S NTH-MGC http://mgc.nci.nih.gov/.

Instinal Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Smith, Ph.D.

Contact: Robert Strausberg, Ph.D.

Contact: Robert Smith, Ph.D.

Contact: Robert S
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                                                                                                                   NIT-MOGO THE TABLE TO TABLE TO TABLE THE TABLE TABLE THE TABLE THE
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/dev stage="s months"
/lab_host="HillDB"
/clone lib="MCI CGAP Mam2"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall; Site="Organ: mammary; Vectorically. Primer: Oligo dT. library constructed by life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 742)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:5371828"
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BQ931041.1 GI:22346072
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                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (japonica cultivar-group)

Edwaryoria, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Edwaryoria, Viridiplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

E (bases 1 to 661)
Jantasuriyarat, C., lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, B.,
Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Context: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 21008B, Tucson, AZ
Fax: 520 621 9288
Fax: 520 621 9288
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/dev_stage="3 week"
/lab_host="DHIOB"
/clone_lib="OSJNE"
/note="Veichor: pBluescript II KS +; Site_1: EcoRI; Site_2:
Xho1; Uninfected Control"
                                                                                                                                                                                    CB681162 661 bp mRNA linear EST 09-APR-2003 OSJNEf07B03.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA clone OSJNEf07B03 5', mRNA sequence.
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Conservative:
Mismatches:
Indels:
322 CGCTGGCCTTGGTGGCCCTGGACGCGGGG 293
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FORMARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Blate: 07 row: B column: 03
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: http://genome.arizona.edu
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Mus musculus (house mouse)
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BI698060
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AGENCOURT 8474869 NIH MGC_129 Mus musculus cDNA clone IMAGE:6310462 BQ715181
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/lab_host="DH10B (phage-resistant)"
/loot=lib=NNH MGC 129"
/host="Corgan: olfactory epithelium; Vector: pCWV-SPORT6.1;
Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 2.2 kb. Constructed
by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
Library."
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov.
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://inage.llnl.gov
Plate: LiAM13732 row: m column: 23
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:6310462"
                                                                                                                                                                                                                                           US-09-444-281-36 (1-12) x BQ877964 (1-959)
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/mol type="minna"
/db xref="taxon:10090"
/clone="IMAGE:507099"
/clone lib="NIH MGC_129"
/clone="Organ: olfactory epithelium; Vector: pGWV-SPORT6.1;
/note="Organ: olfactory epithelium; Vector: pGWV-SPORT6.1;
/note="Organ: olfactory pinner: olfactory profite constructed
primer: oligo dT. Average insert size 2.2 kb. Constructed
by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                          /clone lib="WCI_CGAP Mam2"
/note="Organ: mammary; Vector: pCMV-SPORI6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gibbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:
http://imagel.llnl.gov
Plate: LLAM13724 row: a column: 18
High quality sequence stop: 598.
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 959)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                            /tissue_type="timor, biopsy sample"
/dev_stage="5 months"
/lab_host="DH10B"
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Matches:
Conservative:
Mismatches:
Indels:
http://image.llnl.gov
Plate: LLAM14037 row: c column: 10
High quality sequence stop: 539.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ArgTrpProTrpTrpProTrpArgArgLys 12
                                                                                     1. .946
/organism="Mus musculus"
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/organism="Mus musculus"
                                                                                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:6489249"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-444-281-36 (1-12) x BQ931041 (1-946)
                                                                                                                               /mol_type="mRNA"
/strain="FVB/N-3"
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80.00%
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Best Local Similarity:
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Pred. No.:
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stagleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Bromstein, M.J., Usdin, T.B., Toshiyuki, S., Carnindi, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaranne, P.H., Richards, S.M., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hullyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Burkerley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schwutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences

L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaithersburg, Maryland,
Web site. http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Becketrone.Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,B., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 108 Row: 1 Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6679636 This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R.
Direct Submission
Submitted (11.APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNa Library Preparation: ResGen, Invitrogen Corp
cDNa Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'tissue type="Olfactory epithelium, neonatal mouse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2675
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Contact: MGC help desk
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Conservative:
Mismatches:
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/lab host="DH10B"
/note="Vector: pCMV-SPORT6"
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/organism="Mus musculus"
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/clone="IMAGE:6390348"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 2675)
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Best Local Similarity:
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                                                     BQ715516 1011 bp mRNA linear BST 16-JUL-2002
AGENCOURT_8294996 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6309470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab host="DHION (phage-resistant)"
/clome lab="NIH MGC 129"
/note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
Site-1: BcoRV; Site-2: Not1; Clomed unidirectionally.
Primer: oligo dT. Average insert size 2.2 kb. Constructed
by ResGen, Invitrogen Corp. Note: this is a NIH MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2675 bp mRNA linear HTC 19-NOV-2003 Mus musculus elastin, mRNA (cDNA clone IMAGE:6390348), with EC051074
                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 1011)
NUH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDNA Library Preparation: ResGen. Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://mage.lln.gov
High quality sequence stop: 554.

Location/Qualifiers
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/db_xref="taxon:10090"
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Mus musculus
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BC051074
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Search completed: May 11, 2004, 16:56:35 Job time : 1591.8 secs